

CLAIMS

1 1. A process for altering the host range of.
2 Bacillus toxins which comprises recombining in vitro
3 the variable region of two or more Bacillus toxin genes.

1 2. A process, according to claim 1, wherein the
2 Bacillus is a *Bacillus thuringiensis*.

1 3. A process, according to claim 2, wherein
2 variable regions of Bacillus thuringiensis var.
3 kurstaki HD-1 and Bacillus thuringiensis var.
4 kurstaki HD-73 are recombined in vitro to give genes
5 encoding chimeric toxins having altered host ranges.

1 4. DNA, denoted pEW3, encoding a chimeric toxin
2 having pesticidal activity, as follows:

		(start)	HD-73)		ATG	GATAACAATC	400
3	CGAACATCAA	TGAATGCATT	CCTTATAATT	GTTTAAGTAA	CCCTGAAGTA		
4	GAAGTATTAG	GTGGAGAAAAG	AATAGAAACT	GGTTACACCC	CAATCGATAT	500	
5	TTCCTTGTG	CTAACGCAAT	TTCTTTGAG	TGAATTGTT	CCCGGGTGTG		
6	GATTGTGTT	AGGACTAGTT	GATATAATAT	GGGGAATT	TGGTCCCTCT	600	
7	CAATGGGACG	CATTCTTGT	ACAAATTGAA	CAGTTAATT	ACCAAAGAAT		
8	AGAAGAATT	GCTAGGAACC	AAGCCATTTC	TAGATTAGAA	GGACTAAGCA	700	
9	ATCTTATCA	AATTACGCA	GAATCTTTA	GAGAGTGGGA	AGCAGATCCT		
10	ACTAATCCAG	CATTAAGAGA	AGAGATGCGT	ATTCAATTCA	ATGACATGAA	800	
11	CASTGCCCTT	ACAACCGCTA	TTCCCTTTT	TGCAGTTCAA	AATTATCAAG		
12	TTCCCTTTT	ATCAGTATAT	GTTCAGCCTG	CAAATTACA	TTTATCAGTT	900	
13	TTGAGAGATG	TTTCAGTGT	TGGACAAAGG	TGGGGATTG	ATGCCGCGAC		
14	TATCAATAGT	CGTTATAATG	ATTTAACCTAG	GCTTATTGGC	AACTATACAG	1000	
15	ATTATGCTGT	ACGCTGGTAC	AATACGGGAT	TAGAACGTGT	ATGGGGACCG		
16	GATTCTAGA	ATTGGGTAAG	GTATAATCAA	TTTAAAGAG	AATTAACACT	1100	
17	AACTGTATTA	GATATCGTTG	CTCTGTTCCC	GAATTATGAT	AGTAGAAGAT		
18	ATCCAATTG	AACAGTTCC	CAATTAAACAA	GAGAAATT	TACAAACCCA	1200	
19	GTATTAGAAA	ATTTGTAGG	TAGTTTCA	GGCTCGGCTC	AGGGCATAGA		
20	AAGAAGTATT	AGGAGTCCAC	ATTGTAGGAA	TATACTTAAC	AGTATAACCA	1300	
	TCTATACGGA	TGCTCATAGG	GGTTATTATT	ATTGGTCAGG	GCATCAAATA		
	ATGGCTTCTC	CTGTAGGGTT	TTGGGGGCCA	GAATTCACTT	TTCCGCTATA	1400	
	TGGAACTATG	GGAAATGCAG	CTCCACAAACA	ACGTATTGTT	GCTCAACTAG		
	GTCAGGGCGT	GTATAGAAC	TTATCGTCCA	CTTTATATAG	AAGACCTTT	1500	
	AATATAGGGA	TAATAATCA	ACAACATATCT	GTTCTGACG	GGACAGAATT		
	TGCTTATGGA	ACCTCCTCAA	ATTGCCATC	CGCTGTATAC	AGAAAAAGCG	1600	
	GAACGGTAGA	TTCGCTGGAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA		

21 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTTCGTC 1700
 22 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 23 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 24 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTT 2000
 25 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACAG 2100
 26 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTCA 2200
 27 ACCTTAAGAG TAAATATTAC TGCAACCATT A TCACAAAGAT ATCGGGTAAG 2300
 28 AATTGCGTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG 2400
 29 GAAGACCTAT TAATCAGGGT AATTTTTTCAG CAACTATGAG TAGTGGGAGT 2500
 30 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTAA 2600
 31 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCATT 2700
 32 CAGGCAATGA AGTTTATATA GATCGAATTG AATTGTTCC GGCAGAAGTA 2800
 33 ACCTTGAGG CAGAATATGA TTTAGAAAAGA GCACAAAAGG CGGTGAATGA 2900
 34 GCTGTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT 3000
 35 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATT 3100
 36 TGTCCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG 3200
 37 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 3300
 38 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA 3400
 39 GGAGGCAGTG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 3500
 40 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT 3600
 41 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 3700
 42 GACTTAGAAA TCTATTTAAT TCGCTACAAAT GCAAAACATG AAACAGTAAA 3800
 43 TGTCCTGGGT ACGGGTTCCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 3900
 44 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT 4000
 45 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC C ATCATTCGCA 4100
 46 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC 4200
 47 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 4300
 48 CTAGGGAATC TAGA GTTTCT CGAAGAGAAA CCATTAGTAG GAGAACGCGT 4400
 49 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAT 4500
 50 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT 4600
 51 GCTTTATTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 4700
 52 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAACGTT 4800
 53 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 4900
 54 GAATTAGAAG GGCGTATTTT CACTGCATT TCCTATATG ATGCGAGAAA 5000
 55 TGTCTTAAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 5100
 56 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGTT 5200
 57 CTTCCGGAAT GGGAAAGCAGA AGTGTACACAA GAAGTTCGTG TCTGTCCGGG 5300
 58 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGAA TATGGAGAAG 5400
 59 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 5500
 60 AGCAACTCGG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTTGAA 5600
 61 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 5700
 62 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATT TGCGTCAGTC 5800
 63 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAACATC CTTGTGAATT 5900
 64 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA 6000
 65 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 6100
 66 GAAACGGAAG GAACATTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA 6200
 67 GGAA (end HD-1)

52 and equivalent nucleotide sequences coding for toxin
53 EW3 with the following amino acid sequence:

54

55 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
56 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
57 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
58 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
59 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
60 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
61 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
62 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
63 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
64 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
65 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
66 P E F T F P L Y G T M G N A A P O Q R I V A Q L G Q G V Y R
67 T L S S T L Y R R F F N I G I N N Q Q L S V L D G T E F A Y
68 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
69 P P R O G F S H R L S H V S M F R S G F S N S S V S I I R A
70 P T F S W O H R S A E F N N I I P S S Q I T Q I P L T K S T
71 N L G S B T S V V K G P G F T G G D I L R R T S P G Q I S T
72 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
73 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
74 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
75 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
76 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
77 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
78 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
79 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
80 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
81 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
E N N T D E L K F S N C V E E E I Y F N N T V T C N D Y T V
N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
E E K S Y T D G R R R E N P C E F N R G Y R D Y T P L P V G Y
V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
E L L L M E E.

5. DNA, denoted pEW4, encoding a chimeric toxin, having pesticidal activity, as follows:

(start HD-1) ATGG ATAACAATCC GAACATCAAT 1
 GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
 TGGAGAAAAGA ATAGAAAACGT GTTACACCCC AATCGATATT TCCTTGTGCGC
 TAACGCAATT TCTTTGAGT GAATTGTTC CCGGTGCTGG ATTTGTGTTA 700
 GGACTAGTTG ATATAATATG GGGAAATTGTTT GGTCCCTCTC AATGGGACGC
 ATTTCCGTAA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTG 800
 CTAGGAACCA AGCCATTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
 ATTTACGCAAG AATCTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
 ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
 CAACCGCTAT TCCTCTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTA 1000
 TCACTATATG TTCAAGCTGC AAATTACAT TTATCAGTT TGAGAGATGT
 TTCACTGTTT GGACAAAGGT GGGGATTGTA TGCCGCGACT ATCAATAGTC 1100
 GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
 CGCTGGTACA ATACGGGATT AGAGCGTGTAA TGGGGACCGG ATTCTAGAGA 1200
 TTGGGTAAGG TATAATCAAT TTAGAAAGAGA GCTAACACTT ACTGTATTAG
 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTCGA 1300
 ACAGTTTCCC AATTAACAAG AGAAATTAT GCGAACCCAG TATTAGAAAA
 TTTTGATGGT AGTTTTCGTG GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
 GGCAACCCACA TCTTATGGAT ATCCTTAATA GTATAACCACAT TTATACTGAT
 GTGCATAGAG GCTTTAATTAA TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500
 TGTAGGGTTT TCAGGACCAAG AATTGCAATT CCCTTTATTG GGGAAATGCGG
 GGAATGCAAGC TCCACCCGTA CTTGTCCTCAT TAACTGGTTT GGGGATTTTT 1600
 AGAACATTAT CTTCACCTTT ATATAGAAGA ATTATACTTG GTTCAGGCC
 AAATAATCAG GAACTGTTTG TCCTTGATGG AACGGAGTTT TCTTTGCCT 1700
 CCCTAACGAC CAACTTGCCCT TCCACTATAT ATAGACAAAG GGGTACAGTC
 GATTCACTAG ATGTAAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
 GAGCAGTTA CACCTTGAGA GCTAACGT (stop HD-1)
 (start HD-73) CCT ATGTTCTCTT
 GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
 ACTCAAATCC CTGCAGTGAA GGGAAACTTT CTTTTTAATG GTTCTGTAAT
 TTCAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
 GAAATAACAT TCAGAAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
 TCGACATCTA CCAGATATCG AGTTGCTGTA CGGTATGCTT CTGTAACCCC 2000
 GATTCACCTC AACGTTAATT GGGGTAAATTG ATCCATTGTT TCCAATACAG
 TACCAAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTGGT 2100
 TATTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
 TGTTAGAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200
 TTATTCCAGT TACTGCAACA CTCGAGGGCTG AATATAATCT GGAAAGAGCG
 CAGAAGGGGG TGAATGCGCT GTTTACGTCT ACAAAACCAAC TAGGGCTAAA 2300
 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTGTTACGT
 ATTTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
 GTCAAACATG CGAAGCGACT CAGTGTATGAA CGCAATTAC TCCAAGATT
 AAATTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCGGAAGTA 2500
 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
 ACACTATCAG GTACCTTGA TGAGTGTAT CCAACATATT TGTATCAAAA 2600
 AATCGATGAA TCAAAATTAA AAGCCTTAC CCGTTATCAA TTAAGAGGGT
 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTG CTACAATGCA 2700
 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTTAT GGCGCGCTTT

36 AGCCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCAGCGCCAC 2800
37 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG
38 TGTGCCCATC ATTTCGATCA TTTCTCCCTA GACATTGATG TAGGATGTAC 2900
39 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTAAAG ATTAAGACGC
40 AAGATGGGCA CGCAAGACTA GGGAAATCTAG AGTTTCTCGA AGAGAAACCA 3000
41 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
42 AGACAAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAAAGAGG 3100
43 CAAAAAGAATC TGAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATT
44 CAAGCGGATA CGAATATTGC CATGATTTCAT GCAGGAGATA AACGTGTTCA 3200
45 TAGCATTGCA GAAGCTTATC TGCTCTGAGCT GTCTGTGATT CGGGGTGTCA
46 ATGCAGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTACAC TGCAATTCTCC 3300
47 CTATATGATG CGAGAAAATGT CATTAAAAAT GGTGATTTA ATAATGGCTT
48 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
49 AACGTTCGGT CCTTGTTGTT CGGAAATGGG AAGCAGAAAGT GTCACAAGAA
50 51 GTTCGTGTCT GTCCGGGTGCG TGGCTATATC CTTCGTGTCA CAGCGTACAA 3500
52 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAAATA
53 CAGACGAACG GAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAT 3600
54 AACACGGTAA CGTGTAAATGA TTATACTGTA AATCAAGAAG AATAACGGAGG
55 TGCCTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAAG 3700
56 CTGATTATGCA GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAAGA
57 GAGAATCCTT GTGAATTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
58 AGTTGGTTAT GTGACAAAAAG AATTAGAATA CTTCCCAGAA ACCGATAAGG
59 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTATCGT GGACAGCGTG 3900
60 GAATTACTCC TTATGGAGGA A (end HD-73)

and equivalent nucleotide sequences coding for toxin
EW4 with the following amino acid sequence:

54 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
 55 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 56 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E
 57 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 58 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V
 59 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
 60 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 61 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 62 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N
 63 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L
 64 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G
 65 P E F A F F L F G N A G N A A F P V L V S L T G L G I F R T
 66 L S S P L Y R R I I L G S G P N N Q E L F V L D G T E F S F
 67 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S
 68 V P P R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q
 69 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G
 70 N F L F N G S V I S G P G F T G G D L V R L N S S G N N I Q
 71 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I
 72 H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D
 73 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I
 74 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F
 75 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E
 76 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N
 77 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N
 78 Y V T L S G T F D E C Y P T Y L Y Q K I D E S K L K A F T R
 79 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P
 80 G T G S L W P E S A Q S P I G K C G E P N R C A P H L E W N
 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D
 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E
 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N
 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M
 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F
 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S
 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S
 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H
 E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y
 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S
 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V
 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D
 S V E L L M E E .

1 6. DNA, denoted pACB-1, encoding a chimeric toxin,
 2 having pesticidal activity, as follows:

(start HD-73)				ATG	GATAACAATC	400
3	CGAACATCAA	TGAATGCATT	CCTTATAATT	GTAAAGTAA	CCCTGAAGTA	
4	GAAGTATTAG	GTGGAGAAAG	AATAGAAACT	GGTTACACCC	CAATCGATAT	500
5	TTCCCTGTCG	CTAACGCAAT	TTCTTTGAG	TGAATTGTT	CCCGGTGCTG	
6	GATTGTGTT	AGGACTAGTT	GATATAATAT	GGGGAATT	TGGTCCCTCT	600
7	CAATGGGACG	CATTCTTGT	ACAAATTGAA	CAGTTAATT	ACCAAAGAAT	
8	AGAAGAATT	GCTAGGAACC	AAGCCATTTC	TAGATTAGAA	GGACTAAGCA	700
9	ATCTTATCA	AATTACGCA	GAATCTTTA	GAGAGTGGGA	AGCAGATCCT	
10	ACTAATCCAG	CATTAAGAGA	AGAGATGCGT	ATTCAATTCA	ATGACATGAA	800
11	CAGTGCCTT	ACAACCGCTA	TTCCCTTTT	TGCAGTTCAA	AATTATCAAG	
12	TTCCCTTTT	ATCAGTATAT	GTTCAGSCTG	CAAATTACA	TTTATCAGTT	900
13	TTGAGAGATG	TTTCAGTGT	TGGACAAAGG	TGGGGATT	ATGCCGCGAC	
14	TATCAATAGT	CGTTATAATG	ATTAAC	GCTTATTGGC	AACTATACAG	1000
15	ATTATGCTGT	ACGCTGGTAC	AATA	TAGAACGTGT	ATGGGGACCG	
16	GATTCTAGAG	ATTGGGTAAG	GTATAATCAA	TTTAAAGAG	AATTAAAC	1100
17	AACTGTATTA	GATATCGTT	CTCTGTTCCC	GAATTATGAT	AGTAAAGAT	
18	ATCCAATT	ACAGTTCC	CAATTAACAA	GAGAAATT	TACAAACCCA	1200
19	GTATTAGAA	ATTTGATGG	TAGTTTCGA	GGCTCGGCTC	AGGGCATAGA	
20	AAGAAGTATT	AGGAGTCCAC	ATTGATGGA	TATACTTAA	AGTATAACCA	1300
21	TCTATACGGA	TGCTCATAGG	GGTTATT	ATTGGTCAGG	GCATCAAATA	
22	ATGGCTTCTC	CTGTAGGGTT	TTCCGGGCCA	GAATTCACTT	TTCCGCTATA	1400
23	TGGAAC	GGAAATGCAG	CTCCACAAACA	ACGTATTGTT	GCTCAACTAG	
24	GTCAGGGCGT	GTATAGAAC	TTATCGTCCA	CTTTATATAG	AAGACCTTT	1500
25	AATATAGGG	AAATAATCA	ACAACTATCT	GTTCTTGACG	GGACAGAATT	
26	TGCTTATGGA	ACCTCCTCAA	ATTGCCATC	CGCTGTATAC	AGAAAAAGCG	1600
27	GAACGGTAGA	TTCGCTGAAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA	
28	CCTAGGCAAG	AATTAGTCA	TCGATTAAGC	CATGTTCAA	TGTTCGTTC	1700
29	AGGCTT	AAATAGTAGT	TAAGTATAAT	AAGAGCT	(end hd-73)	
30	(start HD-1)	CCAACGT	TTTCTTGGCA	GCATCGCAGT	1900	
31	GCTGAATT	ATAATATAAT	TCCTTCATCA	CAAATTACAC	AAATACCTT	
32	AACAAAATCT	ACTAATCTT	GCTCTGGAAC	TTCTGTCGTT	AAAGGAC	2000
33	GATTACAGG	AGGAGATATT	CTTCGAAGAA	CTTCACCTGG	CCAGATTCA	
34	ACCTTAAGAG	AAATAATTAC	TGCAACATT	TCACAAAGAT	ATCGGGTAAG	2100
35	AATTGCTAC	GCTTCTACTA	CAAATTACA	ATTCCATACA	TCAATTGACG	
36	GAAGACCTAT	TAATCAGGGT	AATTGTTCA	CAACTATGAG	TAGTGGGAGT	2200
37	AATTACAGT	CCGGAAAGCTT	TAGGACTGT	GGTTTACTA	CTCCGTTAA	
38	CTTTCAAAT	GGATCAAGTG	TATTTACGTT	AAGTGCCTAT	GTCTTCATT	2300
39	CAGGCAATGA	AGTTTATATA	GATCGAATTG	AATTGTTCC	GGCAGAAGTA	
40	ACCTTGAGG	CAGAATATGA	TTAGAAAGA	GCACAAAAGG	CGGTGAATGA	2400
41	GCTGTTACT	TCTTCCAATC	AAATCGGGTT	AAAAACAGAT	GTGACGGATT	
42	ATCATATTGA	TCAAGTATCC	AATTAGTTG	AGTGT	AGATGAATT	2500
43	TGTCTGGATG	AAAAACAAAGA	ATTGTCGAG	AAAGTCAAAC	ATGCGAAGCG	
44	ACTTAGTGT	GAGCGGAATT	TACTTCAGA	TCCAAACTTC	AGAGGGATCA	2600
45	ATAGACAACT	AGACCGTGGC	TGGAGAGGAA	GTACGGATAT	TACCATCAA	
46	GGAGGCGATG	ACGTATTCAA	AGAGAATTAC	GTTACGCTAT	TGGGTACCTT	2700
47	TGATGAGTGC	TATCCAACGT	ATTATATCA	AAAAATAGAT	GAGTCGAAAT	
48	TAAGAGCCTA	TACCGTTAT	CAATTAAGAG	GGTATATCGA	AGATAGTCAA	2800
49	GAATTAGAAA	TCTATTAAAT	TGCTACAA	GCAAAACATG	AAACAGTAAA	
50	TGTGCCAGGT	ACGGGTTCC	TATGGCCGCT	TTCA	AGTCCAATCG	2900
51	GAAAGTGTGG	AGAGCCGAAT	CGATGCGCGC	CACACCTTGA	ATGGAATCCT	
52	GAATTAGATT	GTTCGTGTAG	GGATGGAGAA	AAGTGTGCC	ATCATTGCGCA	3000
53	TCATTCTCC	TTAGACATTG	ATGTTAGGATG	TACAGACTTA	AATGAGGACC	

55 TAGGTGATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 56 CTAGGGAAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 57 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAAT 3200
 58 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 59 GCTTTATTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 60 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 61 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400
 62 GAATTAGAAG GGCCTATTTC CACTGCATTC TCCCTATATG ATGCAGAGAAA
 63 TGTCTTAAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 64 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCCCTGTT
 65 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600
 66 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGG TATGGAGAAG
 67 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700
 68 ABCAACTGCG TAGAAGAGGA AATCTATCCA AATAAACACGG TAACGTGTAA
 69 TGATTATACT GTAAATCAAG AAGAATAACGG AGGTGCGTAC ACTTCTCGTA 3800
 70 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATT TGCGTCAGTC
 71 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAAATC CTTGTGAATT 3900
 72 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 73 AAGAATTAGA ATACTTCCC AAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 74 GAAACGGAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 75 GGAA (end HD-1)

76 and equivalent nucleotide sequences coding for toxin
 77 ACB-1 with the following amino acid sequence:

78 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
 79 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 80 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
 81 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 82 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
 83 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
 84 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 85 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 86 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
 87 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
 88 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
 89 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
 90 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 91 G T T S S N L P S A V Y R K S G T V D S L N E I P P Q N N N V
 92 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A
 93 P T F S W Q H R S A E F N N I P S S Q I T Q I P L T K S T
 94 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 95 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
 96 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G

97 FTTPFNFNSNGSSVFTLSAHVFNNSGNEVYI
98 RIEFVPAEVTFEAEYDLERAQKAVVNELFTS
99 SNQIGLKTDVTDYHIDQVSNLVECLSDDEF
100 LDEKQELSEKVKAHAKRLSDERNLLQDPNF
101 GINRQLDRGWRGSTDITIQQGGDDDVFKENYV
102 TLLGTFDECYPTYLQKIDESKLKAYTRYQ
103 LRGYIEDSQDLEIYLIRYNNAKHETVNVPG
104 GSLWPLSAQSPIGKCGEPNRCAPHLEWNPD
105 LDCSCRDGEEKCAHHSHHFSLDIDVGCTDLN
106 EDLGVWVIFKIKTQDGSHARLGNLEFLEEK
107 LVGEALARVKRAEKWRDKREKLEWETNIIV
108 YKEAKESVDALFVNSQYDQLQADTNIAMIH
109 AADKRVHSIREAYLPELSVIPGVNAAIIFE
110 LEGRIFTAFSLYDARNVIKNGDFNNGLSC
111 NVKGHVVDVEEQNNNQRSVLVLPEWEAEV
112 VRVCPGRGYILRVTAYKEGYGEGCVTIHE
113 ENNTDELKFNSNCVEEEIYPNNNTVTCNDYT
114 NQEELYGGAYTSRNRGYNEAPSVFADYASV
115 EEKSYTDGRRENPCCEFNRGYRDOYTPLPV
116 VTKELEYFPETDKVWIEIGETEGTFIVDS
117 ELLLMEEE.

7. DNA, denoted pSYW1, encoding a chimeric toxin, having pesticidal activity, as follows:

		start	HD-73)	ATG	GATAACAATC	400
3		CGAACATCAA	TGAATGCCATT	CCTTATAATT	GT TTAAGTAA	CCCTGAAGTA
4		GAAGTATTAG	GTGGAGAAAG	AATAGAAACT	GGTTACACCC	CAATCGATAT
5		TTCCTTGTG	CTAACGCAAT	TTCTTTGAG	TGAATTGTT	CCCGGTGCTG
6		GATTTGTGTT	AGGACTAGTT	GATATAATAT	GGGGAATT	TGGTCCCTCT
7		CAATGGGACG	CATTTCTTGT	ACAAATTGAA	CA GT TAATTA	ACCAAAAGAAT
8		AGAAGAATT	GCTAGGAACC	AAGCCATTTC	TAGATTAGAA	GGACTAAGCA
9		ATCTTATCA	AATTTACGCA	GAATCTTTA	GAGAGTGGGA	AGCAGATCCT
10		ACTAATCCAG	CATTAAGAGA	AGAGATGCGT	ATTCAATTCA	ATGACATGAA
11		CAGTGCCCTT	ACAACCGCTA	TTCCCTCTTT	TGCA GTTCAA	AATTATCAAG
12		TTCCCTCTTT	ATCAGTATAT	GTTCAAGCTG	CAAAATTACA	TTTATCAGTT
13		TTGAGAGATG	TTTCAGTGT	TGGACAAAGG	TGGGGATTG	ATGCCGCGAC
14		TATCAATAGT	CGTTATAATG	ATTTAACTAG	GCTTATTGGC	AACTATACAG
15		ATTATGCTGT	ACGCTGGTAC	AATA CGGG GAT	TAGAACGTGT	ATGGGGACCG
16		GATTCTAGAG	ATTGGGTAAG	GTATAATCAA	JTTAGAAGAG	AATTAACACT
17		AACTGTATTA	GATATCGTTG	CTCTGTTCCC	GAATTATGAT	AGTAGAAGAT
18		ATCCAATTG	AACAGTTCC	CAATTAACAA	GAGAAATT	TA CAAACCC A
19		GTATTAGAAA	ATTTTGATGG	TA TTT CGA	GGCTCGGCTC	AGGGCATAGA
20		AGGAAGTATT	AGGAGTCCAC	ATTTGATGGA	TATACTTAAC	AGTATAACCA
21		TCTATACGGA	TGCTCATAAA	<u>GGGG</u> AA ATT T	ATTGGTCAGG	GCATCAAATA
22		ATGGCTTCTC	CTGTAGGGTT	TTCCGGGGCCA	GAATTCACTT	TTCCGCTATA
23		TGGA ACTATG	GGAAATGCAG	CTCCACAAACA	ACGTATTGTT	GCTCAACTAG
24		GTCAGGGCGT	GTATAGAACA	TTATCGTCCA	CTTTATATAG	AAGACCTTTT
25		AATATAAGGGA	TAAATAATCA	ACA ACTATC T	GT TCTTGACG	GGACAGAATT
26						

27 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAAC AGAAAAAAGCG 1600
 28 GAAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 29 CCTAGGCAAG GATTAGTCATCGATTAAGC CATGTTTCAA TGTTTGTTC 1700
 30 AGGCTTTAGT AATAGTAGTG TAAAGTATAAT AAGAGCT (end hd-73)
 31 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 32 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 33 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTGCGTT AAAGGACCAAG 2000
 34 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTCA
 35 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 36 AATTGCTAC GCTTCTACTA CAAATTACA ATTCGATACA TCAATTGACG
 37 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
 38 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTACTA CTCCGTTAA
 39 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCATT 2300
 40 CAGGCAATGA AGTTTATATA GATCGAATTG AATTGTTCC GGCAAGATA
 41 ACCTTTGAGG CAGAATATGA TTTAGAAAAGA GCACAAAAGG CGGTGAATGA 2400
 42 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAAACAGAT GTGACGGATT
 43 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTGTTATC AGATGAATT 2500
 44 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 45 ACTTAGTGTAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
 46 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 47 GGAGGCAGATG ACCTTCAAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 48 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 49 TAAAAGCCTA TACCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 50 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 51 TGTGCCAGGT ACGGGTTCCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 52 GAAAGTGTGG AGAGCCGAAT CGATGCGCAG CACACCTTGA ATGGAATCCT
 53 GACTTAGATT GTTGTGTAG GGATGGAGAA AAGTGTGCCCG ATCATTGCGA 3000
 54 TCATTTCTCC TTAGACATTG ATGAGGATG TACAGACTTA AATGAGGACC
 55 TAGGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 56 CTAGGGAAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 57 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAT 3200
 58 TGGAAATGGGA AACAAATATC GTTGTAAAG AGGCAAAAGA ATCTGTAGAT
 59 GCTTTATTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 60 TGCCTATGATT CATGCGGAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 61 ATCTGCCTGA GCTGTCTGTG ATTCGGGTG TCAATGCGGC TATTTTGAA 3400
 62 GAATTAGAAG GGCCTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 63 TGTCTTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 64 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGTGTT
 65 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCTGTG TCTGTCCGGG 3600
 66 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGGAGGGAA TATGGAGAAAG
 67 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700
 68 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 69 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 70 ATCGAGGATA TAACGAAAGCT CCTTCCGTAC CAGCTGATTG TGCGTCAGTC
 71 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAACATC CTTGTGAATT 3900
 72 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 73 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 74 GAAACGGGAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 75 GGAA (end HD-1)

76 and equivalent nucleotide sequences coding for toxin
77 SYW1 with the following amino acid sequence:

78 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
79 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
80 V D I I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
81 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
82 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
83 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
84 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
85 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
86 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
87 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L
88 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G
89 P E F T F F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
90 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
91 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
92 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
93 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
94 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
95 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
96 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
97 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
98 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
99 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
100 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
101 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
102 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
103 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
104 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
105 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
106 E D L G Y W V I F K I K T Q D G H A R L G N L E F L E E K P
107 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
108 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
109 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
110 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
111 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
112 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
113 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
114 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
115 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
116 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
117 E L L L M E E .

1 8. A chimeric toxin, EW3, having pesticidal
2 activity, having the following amino acid sequence:

3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
12 F V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
13 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
16 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
17 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
19 N L G S G T S V V V K G P G F T G G D I L R R T S P G Q I S T
20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
29 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
31 E D L G V W V I F K I K T Q D G H A P L G N L E F L E E K P
32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
33 Y K E A F E S V P A L F V N S Q Y D O L O A D T N I A M I H
34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
36 N V K G H V D V E E D N N Q R S V L V L P E W E A E V S Q E
37 V R V C P G R G Y I L R V T A Y K E G Y G E G G C V T I H E I
38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
42 E L L L M E E

43 and muteins thercof which do not alter the protein
44 secondary structure.

1 9. A chimeric toxin, EW4, having pesticidal
2 activity, having the following amino acid sequence:

3 MDNNPNIINECIPYNCLSNPPEVEVLGGERIE
4 TGYTPIDISLSLTQFLLSEFVPGAGFVLGL
5 VDIIWGIIFGPSQWDAFPVQIEQLINQRRIEE
6 FARNQAIISRLEGLSNLYQIYAESFREWEAD
7 PTNPFALREEMRIQFNDMNSALTATIPLLA
8 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
9 RWGFDAAATINSRYNDLTRLIGNYTDYAVRW
10 YNTGLERVWGPDSRDWVRYNQFRRELTLTV
11 LDIVALFSNYDSRRYPIRTVSQLTREIYTN
12 PVLENFDGSFRGMAQRIEQNIRQPHLMDIL
13 NSITIYTDVHRGFNYWSGHQITASPVGFSG
14 PEFAFFLFGNAGNAAPPVLVSLTGLGIFRT
15 LSSPLYRRIIILGSGPNNQELFVLDGTEFSF
16 ASLTTLPLSTIYRQRGTVDSLVDVIPPQDNS
17 VPPFRAGFSHRLSHVTMLSQAAGAVYTLRAQ
18 RPMFSWIHRSAEFNNIIASDSITQIPIAVKG
18 NFLFNGSVISGPGFTGGDLLVRLNSSSGNNIQ
20 NRGYIEVPIHFPSNSTSTRYRVRVRYASVTP
21 HLNVNWGNSSIFSNTVPATATSLDNLQSSD
22 FGYFESANAFATSSLGNIVGVRNFSGTAGVI
23 IDRFEFIPVTATLEAEYNLERAQKAVNALF
24 TSTNQLGLKTNVTDYHIDQVSNLVTYLSD
25 FCLDEKRELSEKVKHAKRRLSDERNLLQDSN
26 FKDINRQPGERGGGSTGTTIQQGDDVFKEN
27 YVTLSGTDECYPTYLYQKIDESKLKAFT
28 YQLRGYIEEDSQDLEIYLIYNAKHETVNV
29 GTGSLWPLSAQSPIGKCGEPNRCAPHLEWN
30 PDLDCSCRDGEGKCAHHSHHFSLDDIDVGCT
31 LNEDLGVWVIFKIKTQDGHARLGNLEFLEE
32 KPLVGEALARVKRAEKKWRDKREKLEWETN
33 IVYKEAKESVDAFLVNSQYDQLQADTNIAM
34 IHAADKRVHSIREAYLPELSVIPGVNAAI
35 EELERGRIFTAFSLYDARNVIKNGDFNNGLS
36 CWNVKGHVDVEEQNNQRSQLVVPEWEAEVS
37 QEVRVCPGRGYILRVTAYKEGYGEGCVTIH
38 EIENNNTDELKFNSNCVEEEIYPNNNTVTCNDY
39 TVNQEAEYGGAYTSRNRGYNEAPSVPADYAS
40 VYEEKSYTGDGRRENPCCEFNRGYRDYTPLPV
41 GYVTKELEYFFETDKVWIEIGETEGTFIVD
42 SVELLLMEE

43 and muteins thereof which do not alter the protein
44 secondary structure.

1 10. A chimeric toxin, ACB-1, having pesticidal
2 activity, having the following amino acid sequence:

3 MDNNPNI N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
13 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q Q G V Y R
15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
16 G T S S N L P S A V Y R K S G T V D S L N E I P P Q N N N V
17 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A
18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
29 G S L W F L S A Q S P I G K C G E F N R C A P H L E W N P D
30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
37 V R V C P G R G Y I L R V T A Y K E G Y G E G G C V T I H E I
38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
42 E L L L M E E

43 and muteins thereof which do not alter the protein
44 secondary structure.

1 11. A chimeric toxin, SYW1, having pesticidal
2 activity, having the following amino acid sequence:

3 MDNNPNI N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L
13 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G
14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
16 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
17 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
29 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
30 L D D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
42 E L L L M E E

43 and muteins thereof which do not alter the protein
44 secondary structure.

1 12: A pesticidal composition comprising pesti-
2 cide-containing substantially intact cells having
3 prolonged pesticidal activity when applied to the
4 environment of a target pest, wherein said pesticide,
5 is a chimeric toxin, is intracellular and is produced
6 as a result of expression of a heterologous gene
7 encoding said chimeric toxin in said cell.

1 13. A pesticidal composition according to claim 12,
2 wherein said cells are killed under protease deacti-
3 vating or cell wall strengthening conditions, while
4 retaining pesticidal activity.

1 14. A pesticidal composition, according to claim 12,
2 wherein said cells are prokaryotes selected from the
3 group consisting of Enterobacteriaceae, Bacillaceae,
4 Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudo-
5 monadaceae, Azotobacteraceae, and Nitrobacteraceae; or
6 lower eukaryotes selected from the group consisting
7 of Phycomycetes, Ascomycetes, and Basidiomycetes.

1 15. A pesticidal composition, according to claim 14,
2 wherein said prokaryote is a Bacillus specie selected
3 from a pesticide-producing strain of Bacillus thurin-
4 giensis, consisting of B. thuringiensis M-7, B. thurin-
5 giensis var. kurstaki, B. thuringiensis var. finitimus,
6 B. thuringiensis var. alesti, B. thuringiensis var.
7 sotto, B. thuringiensis var. dendrolimus, B. thurin-
8 giensis var. kenyae, B. thuringiensis var. galleriae,
9 B. thuringiensis var. canadensis, B. thuringiensis var.
10 entomocidus, B. thuringiensis var. subtoxicus, B.
11 thuringiensis var. aizawai, B. thuringiensis var. morri-
12 soni, B. thuringiensis var. ostriniae, B. thuringiensis
13 var. tolworthi, B. thuringiensis var. darmstadiensis,

14 B. thuringiensis var. toumanoffi, B. thuringiensis var.
15 kyushuensis, B. thuringiensis var. thompsoni, B.
16 thuringiensis var. pakistani, B. thuringiensis var.
17 israelensis, B. thuringiensis var. indiana, B. thurin-
18 giensis var. dakota, B. thuringiensis var. tohokuensis,
19 B. thuringiensis var. kumanotoensis, B. thuringiensis
20 var. tochigiensis, B. thuringiensis var. colmeri,
21 B. thuringiensis var. wuhanensis, B. thuringiensis
22 var. tenebrionis, B. thuringiensis var. thuringiensis,
23 and other Bacillus species selected from B. cereus, B.
24 moritai, B. popilliae, B. lentimorbus, and B. sphaericus.

1 16. A method of protecting plants against pests
2 which comprises applying to said plants an effective
3 amount of a pesticidal composition comprising pesti-
4 cide-containing substantially intact unicellular
5 microorganisms, wherein said pesticide is a chimeric
6 toxin, is intracellular, and is produced as a result
7 of expression of a heterologous gene encoding said
8 chimeric toxin in said microorganism, and said micro-
9 organism is treated under conditions which prolong
10 the pesticidal activity when said composition is applied
11 to the environment of a target pest.

1 17. A method according to claim 16, wherein said
2 microorganisms are prokaryotes selected from the
3 group consisting of Enterobacteriaceae, Bacillaceae,
4 Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudo-
5 monadaceae, Azotobacteraceae, and Nitrobacteraceae; or
6 lower eukaryotes, selected from the group consisting
7 of Phycomycetes, Ascomycetes, and Basidiomycetes.

1 18. A method according to claim 16, wherein said
2 unicellular microorganisms are killed under protease
3 deactivating or cell wall strengthening conditions,
4 while retaining pesticidal activity.

1 19. Substantially intact unicellular microorganism
2 cells containing an intracellular chimeric toxin, which
3 toxin is a result of expression of a heterologous
4 gene encoding said chimeric toxin, wherein said cells
5 are killed under protease deactivating or cell wall
6 strengthening conditions, while retaining pesticidal
7 activity when said cell is applied to the environment
8 of a target pest.

1 20. Cells according to claim 19, wherein said
2 microorganism is a Pseudomonad and said toxin is
3 derived from a *B. thuringiensis*.

1 21: A pesticidal composition, according to claim
2 12, wherein said gene, denoted pEW3, encoding a
3 chimeric toxin, is as follows:

		(start	HD-73)	ATG	GATAACAATC	400
4	CGAACATCAA	TGAATGCATT	CCTTATAATT	GT	TTAAGTAA	CCCTGAAGTA
5	GAAGTATTAG	GTGGAGAAAG	AATAGAAA	GG	TTACACCC	CAATCGATAT
6	TTCCTTGTG	CTAACGCAAT	TTCTTTGAG	TGA	ATTGTT	CCCGGTGCTG
7	GATTGTGTT	AGGACTAGTT	GATATAATAT	GGGG	AAATTTT	TGGTCCCTCT
8	CAATGGGACG	CATTTCTTGT	ACAAATTGAA	CAG	TAAATT	ACCAAAGAAT
9	AGAAGAATT	GCTAGGAACC	AAGCCATT	TAG	ATTAGAA	GGACTAAGCA
10	ATCTTATCA	AATTTACGCA	GAATCTTTA	GAG	AGTGGGA	AGCAGATCCT
11	ACTAATCCAG	CATTAAGAGA	AGAGATGCGT	ATT	CAATTCA	ATGACATGAA
12	CAGTGCCCTT	ACAACCGCTA	TTCTCTTT	TG	CAGTTCAA	AATTATCAAG
13	TTCTCTTT	ATCAGTATAT	GTTCAGC	CAA	ATTTACA	TTTATCAGT
14	TTGAGAGATG	TTTCAGTGT	TGGACAAAGG	TTT	GGGATTTG	ATGCCGCGAC
15	TATCAATAGT	CGTTATAATG	ATTTAACTAG	GCTT	TATTGGC	AACTATACAG
	ATTATGCTGT	ACGCTGGTAC	AATACGGGAT	TAGA	ACGTGT	ATGGGGACCG
	GATTCTAGAG	ATTGGGTAAG	GTATAATCAA	TTT	AGAAGAG	AATTAACACT
	AACTGTATT	GATATCGTTG	CTCTGTTCCC	GAATT	TATGAT	AGTAGAAGAT
	ATCCAATTG	AACAGTTCC	CAATTAACAA	GAGAA	ATT	TACAAACCCA
	GTATTAGAAA	ATTTTGATGG	TAGTTT	CGA	GGCTCGGGCTC	AGGGCATAGA

16 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 17 TCTATACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAAATA
 18 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400
 19 TGGAACATATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 20 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTT 1500
 21 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 22 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 23 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 24 CCTAGGCAG GATTTAGTCA TCGATTAAAGC CATGTTCAA TGTTTCGTT 1700
 25 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 26 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900
 27 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 28 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAAG 2000
 29 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTCA
 30 ACCTTAAGAG TAAATATTAC TGCAACATTAA TCACAAAGAT ATCGGGTAAG 2100
 31 AATTGCGTAC GCTTCTACTA CAAATTACAA ATTCCATACAA TCAATTGACG
 32 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
 33 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTACTA CTCCGTTAA
 34 CTTTCAAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 35 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 36 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 37 GCTGTTTACT TCTTCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 38 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATT 2500
 39 TGTCTGGATG AAAAACAAAGA ATTGTCGAG AAAGTCAAAC ATGCGAAGCG
 40 ACTTAGTGAT GAGCGGAATT TACTTCAGA TCCAAACTTC AGAGGGATCA 2600
 41 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 42 GGAGGCAGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 43 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 44 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 45 GACTTAGAAA TCTATTTAAT TCGCTACAAAT GCAAAACATG AAACAGTAAA
 46 TGTGCCAGGT ACGGGTTCTT TATGGCCGCT TTCAGCCCCA AGTCCAATCG 2900
 47 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 48 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCA ATCATTGCA 3000
 49 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTA AATGAGGACC
 50 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 51 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 52 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAT 3200
 53 TGGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 54 GCTTTATTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 55 TGCCATGATT CATGCGCGAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 56 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGSC TATTTTGAA 3400
 57 GAATTAGAAG GGCATTTT CACTGCATTC TCCCTATATG ATGCAGAGAAA
 58 TGTCATTAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 59 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCTTGTGTT
 60 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600
 61 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGAA TATGGAGAAG
 62 GTTGCCTAAC CATTCAATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700
 63 AGCAACTCGC TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 64 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 65 ATCGAGGATA TAACGAAGCT CCTTCCCGTAC CAGCTGATT TGCGTCAGTC
 66 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 67 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 68 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 69 GAAACCGGAAG GAACATTTAT CGTGGACACGC GTGGAAATTAC TCCTTATGGA
 70 GGAA (end HD-1)

52 and equivalent nucleotide sequences coding for toxin
53 EW3 with the following amino acid sequence:

54 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
55 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
56 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
57 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
58 P T N P A L R E E M R I Q F N D M M N S A L T T A I P L F A V
59 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
58 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
59 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
60 L D I V A L F F N Y D S R R Y P I R T V S Q L T R E I Y T N
60 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
61 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
61 P E F T F F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
62 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
63 G T S S N L F P S A V Y R K S G T V D S L D E I P P Q N N N V
63 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
64 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
65 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
65 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
66 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
67 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
67 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
68 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
69 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
69 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
70 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
71 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
71 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
72 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
72 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
73 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
74 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
74 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
75 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
76 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
77 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
77 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
78 N Q E E Y G G A Y T S R N R G Y N E A F S V P A D Y A S V Y
78 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
79 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
80 E L L L M E E.

1 22. A pesticidal composition, according to claim
2 12, wherein said gene, denoted pEW4, encoding a
3 chimeric toxin, is as follows:

4	(start HD-1)		ATGG	ATAACAATCC	GAACATCAAT	
5	GAATGCATTC	CTTATAATTG	TTTAAGTAAAC	CCTGAAGTAG	AAGTATTAGG	600
6	TGGAGAAAGA	ATAGAAAATCG	GTACACCCCC	AATCGATATT	TCCTTGTGCG	
7	TAACCGAATT	TCTTTGAGT	GAATTTGTT	CCGGTGTCTGG	ATTTGTGTTA	700
8	GGACTAGTTG	ATATAATATG	GGGAATTTTT	GGTCCCTCTC	AATGGGACGC	
9	ATTTCCGTGA	CAAATTGAAC	AGTTAATTAA	CCAAAAGAATA	GAAGAATTTCG	800
10	CTAGGAACCA	AGCCATTCT	AGATTAGAAG	GACTAAGCAA	TCTTTATCAA	
11	ATTTACGCGAG	AATCTTTAG	AGAGTGCGAA	GCAGATCCTA	CTAATCCAGC	900
12	ATTAAGAGAA	GAGATGCGTA	TTCATTCAA	TGACATGAAC	AGTGCCCTTA	
13	CAACCGCTAT	TCCTCTTTG	GCAGTTCAAA	ATTATCAAGT	TCCTCTTTA	1000
14	TCAGTATATG	TTCAAGCTGC	AAATTACAT	TTATCAGTTT	TGAGAGATGT	
15	TTCAGTGTGTT	GGACAAAGGT	GGGGATTGAA	TGCCGCGACT	ATCAATAGTC	1100
16	GTTATAATGA	TTTAACCTAGG	CTTATTGCGA	ACTATACAGA	TTATGCTGTG	
17	CGCTGGTACA	ATACGGGATT	AGAGCGTGTA	TGGGGACCGG	ATTCTAGAGA	1200
18	TTGGGTAAGG	TATAATCAAT	TTAGAAGAGA	GCTAACACTT	ACTGTATTAG	
19	ATATCGTTGC	TCTATTCTCA	AATTATGATA	GTCGAAGGTA	TCCAATTGCGA	1300
20	ACAGTTTCCC	AATTAAACAAG	AGAAAATTAT	ACGAACCCAG	TATTAGAAAA	
21	TTTTGATGGT	AGTTTCTGT	GAATGGCTCA	GAGAATAGAA	CAGAATATTA	1400
22	GGCAACCACA	TCTTATGGAT	ATCCTTAATA	GTATAACCAT	TTATACGTAT	
23	GTGCATAGAG	GCTTTAATTA	TTGGTCAGGG	CATCAAATAA	CAGCTTCTCC	1500
24	TGTAGGGTTT	TCAGGACCAAG	AATTGCGATT	CCCTTTATT	GGGAATGCGG	
25	GGAATGCGC	TCCACCCGTA	CTTGTCTCAT	TAACTGGTTT	GGGGATTTTT	1600
26	AGAACATTAT	CTTCACCTTT	ATATAGAAGA	ATTATACCTG	GTTCAGGCC	
27	AAATAATCG	GAACGTGTTG	TCCCTGATGG	AACGGAGTTT	TCTTTGCGCT	1700
28	CCCTAACGAC	CAACTTGCT	TCCACTATAT	ATAGACAAAG	GGGTACAGTC	
29	GATTCACTAG	ATGTAATACC	GCCACAGGAT	AATAGTGTAC	CACCTCGTGC	1800
	GGGATTTCAGC	CATCGATTGA	GTCATGTTAC	AATGCTGAGC	CAAGCAGCTG	
	GAGCAGTTA	CACCTTGAGA	GCTCAACGT	(stop HD-1)		
	(start HD-73)		CCT	ATGTTCTCTT		
30	GGATACATCG	TAGTGCTGAA	TTTAATAATA	TAATTGCATC	GGATAGTATT	1800
31	ACTCAAATCC	CTGCAGTGA	GGGAAACCTT	CTTTTTAATG	GTTCGTAA	
32	TTCAGGACCA	GGATTTACTG	GTGGGGACTT	AGTTAGATTA	AATAGTAGTG	1900
33	GAAATAACAT	TCAGAATAGA	GGGTATATTG	AAGTCCAAAT	TCACTTCCCA	
34	TCGACATCTA	CCAGATATCG	AGTTCTGTGA	CGGTATGCTT	CTGTAACCCCC	2000
35	GATTACACCTC	AACGTTAATT	GGGGTAATT	ATCCATT	TCCAATACAG	
36	TACCAAGCTAC	AGCTACGTCA	TTAGATAATC	TACAATCAAG	TGATTTGGT	2100
37	TATTTGAAA	GTGCGCAATGC	TTTTACATCT	TCATTAGGTA	ATATAGTAGG	
38	TGTTAGAAAT	TTTAGTGGGA	CTGCAGGAGT	GATAATAGAC	AGATTTGAAT	2200
39	TTATTCCAGT	TACTGCAACA	CTCGAGGCTG	AATATAATCT	GGAAAGAGCG	

30 CAGAAGGCAGG TGAATGCGCT GTTTACGTCT ACAAAACCAAC TAGGGCTAAA 2300
 31 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
 32 ATTTATCGGA TGAATTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
 33 GTCAAACATG CGAAGCGACT CAGTGTGAA CGCAATTAC TCCAAGATTC
 34 AAATTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCGGAAGTA 2500
 35 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
 36 ACACTATCAG GTACCTTGA TGAGTGTCTAT CCAACATATT TGTATCAAAA 2600
 37 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT
 38 ATATCGAAGA TAGTCAAGAC TTAGAAAATCT ATTTAATTG TGACAAATGCA 2700
 39 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTTAT GGCCGCTTTC
 40 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCGCGCCAC 2800
 41 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAAG
 42 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900
 43 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 44 AAGATGGGCA CGCAAGACTA GGGAACTAG AGTTTCTCGA AGAGAAACCA 3000
 45 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 46 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAAGAGG 3100
 47 CAAAAGAATC TGTAGATGCT TTATTTGAA ACTCTCAATA TGATCAATTA
 48 CAAGCGGATA CGAATATTGC CATGATTCAAT GCGGCAGATA AACGTGTTCA 3200
 49 TAGCATTCGA GAAGCCTTATC TGCCCTGAGCT GTCTGTGATT CGGGGTGTCA
 50 ATGCGGCTAT TTTGAAAGAA TTAGAAGGGC GTATTTTCAC TGCAATTCTCC 3300
 51 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTA ATAATGGCTT
 52 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 53 AACGTTCGST CCTTGTGTT CCGGAATGGG AAGCAGAAGT GTCACAAAGAA
 54 GTTCGTGTCT GTCCGGGTG TGCTATATC CTTCGTGTCA CAGCGTACAA 3500
 55 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAAATA
 56 CAGACGAACG GAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAAT 3600
 57 AACACGGTAA CGTGTAAATGA TTATACTGTA AATCAAGAAG AATACGGAGG
 58 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCT TCCGTACCAAG 3700
 59 CTGATTATGC GTCACTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 60 GAGAATCCTT GTGAATTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 61 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCCAGAA ACCGATAAGG
 62 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTATCGT GGACAGCGTG 3900
 63 GAATTACTCC TTATGGAGGA A (end HD-73)

52 and equivalent nucleotide sequences coding for toxin
 53 EW4 with the following amino acid sequence:

54 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
 55 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 56 V D I I W G I F G P S Q W D A F F P V Q I E Q L I N Q R I E E
 57 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 58 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V
 59 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q
 60 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 61 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 62 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N
 63 F V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L
 64 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G
 65 P E F A F P L F G N A G N A A P P V L V S L T G L G I F R T

62 L S S P L Y R R I I L G S G P N N Q E L F V L D G T E F S F
63 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S
64 V P P R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q
65 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G
66 N F L F N G S V I S G P G F T G G D L V R L N S S G N N I Q
67 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I
68 H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D
69 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I
70 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F
71 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E
72 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N
73 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N
74 Y V T L S G T F D E C Y P T Y L Y Q K I D E S K L K A F T R
75 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P
76 G T G S L W P L S A Q S P I G K C G E P N R C A P H L E W N
77 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D
78 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E
79 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N M
80 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M
81 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F
82 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S
83 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S
84 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H
85 E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y S
86 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S
87 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V
88 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D
89 S V E L L L M E E .

1 23. A pesticidal composition, according to claim
2 12, wherein said gene, denoted pACB-1, encoding a
3 chimeric toxin, is as follows:

	(start HD-73)		ATG	GATAACAATC	400
4	CGAACATCAA	TGAATGCATT	CCTTATAATT	GTAAAGTAA	CCCTGAAGTA
5	GAAGTATTAG	GTGGAGAAAG	AATAGAAACT	GGTTACACCC	CAATCGATAT
6	TTCCCTGTG	CTAACGCAAT	TTCTTTGAG	TGAATTGTT	CCCGGTGCTG
7	GATTTGTGTT	AGGACTAGTT	GATATAATAT	GGGGAAATT	TGGTCCCTCT
8	CAATGGGACG	CATTCTTGT	ACAAATTGAA	CAGTTAATT	ACCAAAGAAT
9	AGAAGAATT	GCTAGGAACC	AAGCCATTTC	TAGATTAGAA	GGACTAAGCA
10	ATCTTATCA	AATTACGCA	GAATCTTTA	GAGAGTBGGA	AGCAGATCCT
11	ACTAATCCAG	CATTAAGAGA	AGAGATGCGT	ATTCAATTCA	ATGACATGAA
12	CAGTGCCCTT	ACAACCGCTA	TTCCCTTTT	TGCAAGTCAA	AATTATCAAG
13	TTCCCTTTT	ATCAGTATAT	GTTCAAGCTG	CAAATTACA	TTTATCAGTT
14	TTGAGAGATG	TTTCAGTGT	TGGACAAAGG	TGGGGATTG	ATGCCGCGAC
15					

16 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 17 ATTATGCTGT ACGCTGGTAC AATAACGGGAT TAGAACGTGT ATGGGGACCG
 18 GATTCTAGAG ATTGGGTAAG STATAATCAA TTTAGAAGAG AATTAACACT 1100
 19 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 20 ATCCAATTG AACAGTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200
 21 STATTAGAAA ATTTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA
 22 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 23 TCTATAACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAAATA
 24 ATGGCTTCTC CTGTAAGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400
 25 TGGAACTATG GGAAATGCAG CTCCACAAACA ACGTATTGTT GCTCAACTAG
 26 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTT 1500
 27 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 28 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAAGCG 1600
 29 GAACGGTAGA TTCGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA
 30 CCTAGGCAAG AATTAGTCA TCGATTAAGC CATGTTCAA TGTTCGTTC 1700
 31 AGGCTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 32 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 33 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTT
 34 AACAAAAATCT ACTAATCTTG BCTCTGGAAC TTCTGTCGTT AAAGGACCG 2000
 35 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTC
 36 ACCTTAAGAG TAAATATTAC TGCAACATTA TCACAAAGAT ATCGGGTAAG 2100
 37 AATTGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 38 GAAGACCTAT TAATCAGGTT AATTTCAG CAACTATGAG TAGTGGGAGT 2200
 39 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTAA
 40 CTTTCAAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT STCTTCATT 2300
 41 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 42 ACCTTTGAGG CAGAATATGA TTAGAAAAGA GCACAAAAGG CGGTGAATGA 2400
 43 GCTGTTTACT TCTTCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 44 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTGTTATC AGATGAATT 2500
 45 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 46 ACTTAGTGT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
 47 ATAGACAACG AGACCGTGSC TGGAGAGGAA GTACGGATAT TACCATCCAA
 48 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 49 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 50 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTC 2800
 51 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 52 TGTGCCAGGT ACGGGTTCCCT TATGGCCGCT TTCAAGCCAA AGTCCAATCG 2900
 53 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 54 GACTTAGATT GTTGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTCGCA 3000
 55 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGGACC
 56 TAGGTGTATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 57 CTAGGGAAATC TAGAGTTCTC CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 58 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAT 3200
 59 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 60 GCTTTATTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 61 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 62 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400
 63 GAATTAGAAG GGCCTATTG CACTGCATTG TCCCTATATG ATGCGAGAAA
 64 TGTCACTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 65 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCCCTGTT

66 CTTCCCGAAT GGGAAAGCAGA AGTGTACCAA GAAGTTCTTG TCTGTCCGGG 3600
 67 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGG TATGGAGAAG
 68 GTTGCCTAAC CATTGATGAG ATCGAGAAACA ATACAGACGA ACTGAAGTTT 3700
 69 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 70 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCCTAC ACTTCTCGTA 3800
 71 ATCGAGGATA TAACGAAGCT CCTTCCCGTAC CAGCTGATTAA TGCCTCAGTC
 72 TATGAAGAAA AATCGTATAAC AGATGGACGA AGAGAGAAATC CTTGTGAATT 3900
 73 TAACAGAGGG TATAAGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 74 AAGAATTAGA ATACTTCCC AAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 75 GAAACGGAAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 76 GGAA (end HD-1)

77 and equivalent nucleotide sequences coding for toxin
 78 ACB-1 with the following amino acid sequence:

79 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
 80 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 81 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
 82 F A R N Q A I S . R L E G L S N L Y Q I Y A E S F R E W E A D
 83 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
 84 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
 85 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 86 Y N . T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 87 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
 88 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
 89 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
 90 P E F T F P L Y . G T M G N A A P Q Q R I V A Q L G Q G V Y R
 91 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 92 G T S S N L P S A V Y R K S G T V D S L N E I P P Q N N N V
 93 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A
 94 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
 95 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 96 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
 97 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
 98 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
 99 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
 100 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
 101 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
 102 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
 103 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
 104 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
 105 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
 106 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
 107 E D L G Y W V I F K I K T Q D G H A R L G N L E F L E E K P
 108 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
 109 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
 110 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E

111 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
 112 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
 113 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
 114 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
 115 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
 116 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
 117 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
 118 E L L L M E E.

1 24. A pesticidal composition, according to
 2 claim 12, wherein said gene, denoted pSYW1, encoding
 3 a chimeric toxin, is as follows:

4 (start HD-73) ATG GATAACAATC 400
 5 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 6 GAAGTATTAG GTGGAGAAAG AATAGAAAATC GGTTACACCC CAATCGATAT 500
 7 TTCCCTTGTGCG CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGCTG
 8 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGSTCCCTCT 600
 9 CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAATTA ACCAAAGAAT
 10 AGAAGAATTG GCTAGGAACG AAGCCATTTC TAGATTAGAA GGACTAAGCA 700
 11 ATCTTATCA AATTACGCA GAAATCTTTA GAGAGTGGGA AGCAGATCCT
 12 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 13 CAGTGCCCTT ACAACCGCTA TTCCCTTTT TGCAAGCTG CAAATTTACA AATTATCAAG
 14 TTCCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 15 TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTG ATGCCGCGAC
 16 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 17 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 18 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAAACACT 1100
 19 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 20 ATCCAATTG AACAGTTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200
 21 GTATTAGAAA ATTTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAAGA
 22 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 23 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAAATA
 24 ATGGCTTCTC CTGTTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400
 25 TGGAACTATG GGAAATGCGAG CTCCACAAACA ACGTATTGTT GCTCAACTAG
 26 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 27 AATATAGGGAA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 28 TGCTTATGGAA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 29 GAAACGGTAGA TTGCGTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 30 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTTGTTC 1700
 31 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 32 (start HD-1) CCAACGT TTTCTGGCA GCATCGCACT 1900
 33 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 34 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCG 2000
 35 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTCA
 36 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 37 AATTGCGTAC GCTTCTACTA CAAATTACA ATTCCATACA TCAATTGACG
 38 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
 39 AATTTACAGT CGGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTAA
 40 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCATT 2300
 41 CAGGCAATGA AGTTTATATA GATCBAATTG AATTTGTTCC GGCAGAAAGTA

42 ACCTTTGAGG CAGAATATGA TTTAGAAAAGA GCACAAAAGG CGGTGAATGA 2400
43 GCTGTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
44 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATT 2500
45 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
46 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
47 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
48 GGAGGCAGTG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
49 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
50 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
51 GACTTAGAGAA TCTATTAAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
52 TGTGCCAGGT ACGGGTTCTT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
53 GAAAGTGTGG AGAGCCGAAT CGATGCGCAGC CACACCTTGA ATGGAATCCT
54 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCA 3000
55 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
56 TAGGTGTATG BGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
57 CTAGGGAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
58 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAT 3200
59 TGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
60 GCTTTATTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
61 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCCTT
62 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTGGAA 3400
63 GAATTAGAAG GGCCTATTT CACTGCATTC TCCCTATATG ATGCGAGAAA
64 TGTCATTAAG AATGGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
65 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCCCTGTT
66 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600
67 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGGAGGGG TATGGAGAAG
68 GTTGCCTAAC CATTCAATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700
69 AGCAACTGCG TAGAAGAGGA AATCTATCAA AATAACACGG TAACGTGTAA
70 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
71 ATCGAGGATA TAACGAAAGCT CCTTCCGTAC CAGCTGATT TGCGTCAGTC
72 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAAATC CTTGTGAATT 3900
73 TAACAGAGGG TATAGGGATT ACACGCAACT ACCAGTTGGT TATGTGACAA
74 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
75 GAAACCGGAAG GAACATTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA
76 GGAA (end HD-1)

77 and equivalent nucleotide sequences coding for toxin
78 SYW1 with the following amino acid sequence:

79 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
80 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
81 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
82 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
83 P T N P A L R E E M R I Q F N D M N S A L T T A I F L F A V
84 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
85 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
86 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
87 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
88 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L
89 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G
90 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R

91 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y .
92 G T S S N L F S A V Y R K S G T V D S L D E I P P Q N N N V
93 P P . R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
94 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
95 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
96 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
97 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
98 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
99 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
100 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
101 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
102 S I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
103 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
104 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
105 G S L W P L S A Q S P I G K C G E F P N R C A P H L E W N P D
106 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
107 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
108 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
109 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
110 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
111 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
112 N V . K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
113 V R . V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
114 E N N T D E L K F S N C V E E E I Y P N N N T V T C N D Y T V
115 N Q E E Y G G A Y T S R . N R G Y N E A P S V P A D Y A S V Y
116 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L R V G Y
117 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
118 E L L L M E E .

1 25. A recombinant DNA transfer vector comprising
2 DNA having the following nucleotide sequence or
3 equivalent nucleotide sequences containing bases whose
4 translated region codes for the same amino acid sequence:

		(start HD-73)	ATG	GATAACAATC	400
5	CGAACATCAA	TGAATGCATT	CCTTATAATT	GTTTAAGTAA	CCCTGAAGTA
6	GAAGTATTAG	GTGGAGAAAG	AATAGAAACT	GGTTACACCC	CAATCGATAT
7	TTCCTTGTG	CTAACGCAAT	TTCTTTGAG	TGAATTGTT	CCCGGTGCTG
8	GATTGTGTT	AGGACTAGTT	GATATAATAT	GGGGAATT	TGGTCCCTCT
9	CAATGGGACG	CATTCTTGT	ACAAATTGAA	CAGTTAATT	ACCAAAGAAT
10	AGAAGAATT	GCTAGGAACC	AAGCCATTTC	TAGATTAGAA	GGACTAAGCA
11	ATCTTATCA	AATTACGCA	GAATCTTTA	GAGAGTGGGA	AGCAGATCCT
12	ACTAATCCAG	CATTAAGAGA	AGAGATGCGT	ATTCAATTCA	ATGACATGAA
13	CAGTGCCCTT	ACAACCGCTA	TTCCCTCTTT	TGCAGTTCAA	AATTATCAAG
14	TTCCCTCTTT	ATCAGTATAT	GTCAAGCTG	CAAATTACA	TTTATCAGTT
15	TTGAGAGATG	TTTCAGTGT	TGGACAAAGG	TGGGGATTG	ATGCCCGGAC
16	TATCAATAGT	CGTTATAATG	ATTTAACTAG	GCTTATTGGC	AACTATACAG
17	ATTATGCTGT	ACGCTGGTAC	AATACGGGAT	TAGAACGTG	ATGGGGACCG
18	GATTCTAGAG	ATTGGGTAAG	GTATAATCAA	TTTAGAAGAG	AATTAAACACT
19	AACTGTATTA	GATATCGTTG	CTCTGTTCCC	GAATTATGAT	AGTAGAAGAT
20	ATCCAATTG	AACAGTTCC	CAATTAAACAA	GAGAAATT	TACAAACCCA
21	GTATTAGAAA	ATTTGATGG	TAGTTTCGA	GGCTCGGCTC	AGGGCATAGA
22					

23 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 24 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA
 25 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400
 26 TGGAACTATG GGAAATGCAG CTCCACAAACA ACGTATTGTT GCTCAACTAG
 27 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTT 1500
 28 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 29 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 30 GAACGGTAGA TTCGCTGGAT GAAATACCAG CACAGAAATAA CAACGTGCCA
 31 CCTAGGCAAG GATTAGTCA TCGATTAAGC CATGTTTCAA TGTTCGTTC 1700
 32 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 33 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900
 34 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTT
 35 AACAAAATCT ACTAATCTTG GCTCTGAAAC TTCTGTCGTT AAAGGACCAAG 2000
 36 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTC
 37 ACCTTAASAG TAAATATTAC TGCAACCATTA TCACAAAGAT ATCAGGTAAG 2100
 38 AATTGCGTAC GCTTCTACTA CAAATTACA ATTCCATACA TCAATTGACG
 39 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
 40 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTAA
 41 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCATT 2300
 42 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 43 ACCTTTGAGG CAGAATATGA TTTAGAAAAGA GCACAAAAGG CGGTGAATGA 2400
 44 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 45 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTGTTATC AGATGAATT 2500
 46 TGTCTGGATG AAAAACAAAGA ATTGTCGAG AAAGTCAAAC ATGCGAAGCG
 47 ACTTAGTGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
 48 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 49 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 50 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 51 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 52 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 53 TGTGCCAGGT ACGGGTTCTC TATGCCCGCT TTCAGCCCCA AGTCCAATCG 2900
 54 GAAAAGTGTGG AGAGCGAAT CGATCGCGC CACACCTTGA ATGGAATCCT
 55 GACTTAGATT GTTCGTTGAG GGATGGAGAA AAGTGTGCCC ATCATTGCA 3000
 56 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 57 TAGGTGTATG BGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 58 CTAGGGAATC TAGAGTTCTC CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 59 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 60 TGGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 61 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 62 TGCCATGATT CATGCGGCAG ATAAACGTGT TCAATAGCATT CGAGAAAGCTT
 63 ATCTGCCTGA GCTGCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400
 64 GAATTAGAAG GGCATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 65 TGTCAATTAA AATGGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 66 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGTT
 67 CTTCCGGAAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600
 68 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGG TATGGAGAAG
 69 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700
 70 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 71 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 72 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATT TGCGTCAGTC
 73 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 74 TAACAGAGGG TATAGGGATT ACACGCGACT ACCAGTTGGT TATGTGACAA
 75 AAGAATTAGA ATACTTCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 76 GAAACGGGAAG GAACATTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA
 77 GGAA (end HD-1).

1 26. A recombinant DNA transfer vector comprising
2 DNA having the following nucleotide sequence or
3 equivalent nucleotide sequences containing bases whose
4 translated region codes for the same amino acid sequence:

5 (start HD-1) ATGG ATAACAAATCC GAACATCAAT
6 GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
7 TGGAGAAAAA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTGCGC
8 TAACGCAATT TCTTTGAGT GAATTGTTTC CCGGTGCTGG ATTTGTGTTA 700
9 GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC
10 ATTTCCTGTA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTG 800
11 CTAGGAACCA AGCCATTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
12 ATTTACGCGAG AATCTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
13 ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
14 CAACCGCTAT TCCTCTTTG GCAGTTCAA ATTATCAAGT TCCTCTTTA 1000
15 TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTT TGAGAGATGT
16 TTCAGTGTGTT GGACAAAGGT GGGGATTGTA TGCCGCGACT ATCAATAGTC 1100
17 GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
18 CGCTGGTACA ATACGGGATT AGAGCGTGTG TGGGGACCGG ATTCTAGAGA 1200
19 TTGGGTAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
20 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTGCA 1300
21 ACAGTTTCCC AATTAACAAG AGAAATTAT AGCAACCCAG TATTAGAAAA
22 TTTGATGGT AGTTTCGTG GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
23 GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCATT TTATACTGAT
24 GTGCATAGAG GCTTTAATTG TTGGTCAGGG CATCAAATAA CAGCTCTCC 1500
25 TGTAGGGTTT TCAGGACCAAG AATTGCGATT CCCTTTATTG GGGAAATGCGG
26 GGAATGCAGC TCCACCCCGTA CTTGTCTCAT TAACTGGTTT GGGGATTTTT 1600
27 AGAACATTAT CTTCACCTT ATATAGAAGA ATTATACTTG GTTCAGGGCCC
28 AAATAATCAG GAACTGTTTG TCCTTGATGG AACGGAGTTT TCTTTTGCCCT 1700
29 CCCTAACGAC CAACTTGCCCT TCCACTATAT ATAGACAAAG GGGTACAGTC
30 GATTCACTAG ATGTAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
31 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
32 GAGCAGTTA CACCTTGAGA GCTCAACGT (stop HD-1)
33 (start HD-73) CCT ATGTTCTCTT
34 GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCAATC GGATAGTATT 1800
35 ACTCAAATCC CTGCACTGAA GGGAAACTTT CTTTTTAATG GTTCTGTAAT
36 TTCAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
37 GAAATAACAT TCAGAAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
38 TCGACATCTA CCAGATATCG AGTTCGTGTG CGGTATGCTT CTGTAACCCC 2000
39 GATTCACCTC AACGTTAATT GGGGTAATTC ATCCATTGTT TCCAATACAG
40 TACCAAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTGGT 2100
41 TATTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATACTAGG
42 TGTTAGAAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTGAAAT 2200
43 TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG
44 CAGAAGGCGG TGAATGCGCT GTTACGCTC ACAAAACCAAC TAGGGCTAAA 2300
45 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
46 ATTATCGGA TGAATTGTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
47 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTAC TCCAAGATTC
48 AAATTTCAA GACATTAATA GGCAACCCAGA ACGTGGGTGG GGCAGGAAGTA 2500
49 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
50 ACACTATCAG GTACCTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600
51 AATCGATGAA TCAAAATTAA AAGCCTTAC CCGTTATCAA TTAAGAGGGT

52 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTG 2700
 53 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTCCTTAT GGCGCTTC
 54 AGCCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCAGCGCCAC 2800
 55 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGAA TGGAGAAAAG
 56 TGTGCCCATC ATTGCGATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900
 57 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 58 AAGATGGGCA CGCAAGACTA GGGAACTCTAG AGTTTCTCGA AGAGAAACCA 3000
 59 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAATGGAG
 60 AGACAAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAAGAGG 3100
 61 CAAAAGAATC TGAGATGCT TTATTTGTAAC ACTCTCAATA TGATCAATTA
 62 CAAGCGGATA CGAATATTGC CATGATTCA GCGGCAGATA AACGTGTTCA 3200
 63 TAGCATTGCA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CGGGGTGTCA
 64 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300
 65 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT
 66 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 67 AACGTTCGGT CCTTGTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
 68 GTTCGTGTCT GTCCGGGTG TGCTATATC CTTCTGTGTC CAGCGTACAA 3500
 69 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAAATA
 70 CAGACGAACG GAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAAT 3600
 71 AACACGGTAA CGTGTAAATGA TTATACGTAA AATCAAGAAG AATACGGAGG
 72 TGCCTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAAG 3700
 73 CTGATTATGTC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 74 GAGAACCTT GTGAATTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 75 AGTTGGTTAT GTGACAAAG AATTAGAATA CTTCCCAGAA ACCGATAAGG
 76 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTATCGT GGACAGCGTG 3900
 77 GAATTACTCC TTATGGAGGA A (end HD-73).

1 27. A recombinant DNA transfer vector comprising
 2 DNA having the following nucleotide sequence or
 3 equivalent nucleotide sequences containing bases whose
 4 translated region codes for the same amino acid
 5 sequence:

6 (start HD-73) ATG GATAACAATC 400
 7 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 8 GAAGTATTAG GTGGAGAAAG AATAGAAAATC GGTTACACCC CAATCGATAT 500
 9 TTCTTGTGCG CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGCTG
 10 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 11 CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAATTA ACCAAAGAAT
 12 AGAAGAATTG CTAGGAAACC AAGCCATTTC TAGATTGAA GGACTAAGCA 700
 13 ATCTTATCA AATTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT
 14 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 15 CAGTGCCCTT ACAACCGCTA TTCCCTTTTG TGCAAGTCAA AATTATCAAG
 16 TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTACAA TTTATCAGTT 900
 17 TTGAGAGATG TTTCAGTGTGTT TGGACAAAGG TGGGGATTG ATGCCGCGAC
 18 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 19 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 20 GATTCTAGAS ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAAACACT 1100
 21 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAAAGAGT

22 ATCCAATTG AACAGTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200
 23 GTATTAGAAA ATTTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA
 24 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 25 TCTATACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAAATA
 26 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400
 27 TGGAACATATG GGAAATGCAG CTCCACAAACA ACGTATTGTT GCTCAACTAG
 28 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 29 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 30 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 31 GAACGGTAGA TTCGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA
 32 CCTAGGGCAAG AATTTAGTCA TCGATTAAAGC CATGTTTCAA TGTTTCGTT 1700
 33 AGGCTTGTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 34 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900
 35 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 36 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 37 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTCA
 38 ACCTTAAGAG TAAATATTAC TGCAACATTA TCACAAAGAT ATCAGGGTAAG 2100
 39 AATTCGCTAC GCTTCTACTA CAAATTACA ATTCCATACA TCAATTGACG
 40 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
 41 AATTTACAGT CCGGAAGCTT TAGGACTGTA GTTTTACTA CTCCGTTAA
 42 CTTTTCAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCATT 2300
 43 CAGGCAATGA AGTTTATATA GATCBAATTG AATTTGTTCC GGCAGAAGTA
 44 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 45 GCTGTTTACT TCTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 46 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTGTTATC AGATGAATT 2500
 47 TGCTGGATG AAAAACAAAGA ATTGTCGAG AAAGTCAAAC ATGCGAAGCG
 48 ACTTAGTGAT GAGCGGAATT TACTTCAGA TCCAAACTTC AGAGGGATCA 2600
 49 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 50 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 51 TGATGAGTGC TATCCAACGT ATTTATATCA AAAATAGAT GAGTCGAAAT
 52 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 53 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 54 TGTGCCAGGT ACGGGTTCCCT TATGGCCGCT TTCAGCCCCA AGTCCAATCG 2900
 55 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 56 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC ATCATTCGCA 3000
 57 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 58 TAGGTGTATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 59 CTAGGGAAATC TAGAGTTCT CGAAGAGAAA CATTAGTAG GAGAAGCGCT
 60 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 61 TGGAAATGGGA AACAAATATC GTTTATAAG AGGCAAAAGA ATCTGTAGAT
 62 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 63 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 64 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400
 65 GAATTAGAAG GGCCTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 66 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 67 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCCCTGTT
 68 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTT TCTGTCCGGG 3600
 69 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGGAGGGA TATGGAGAAG
 70 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700
 71 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA

72 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCCTAC ACTTCTCGTA 3800
 73 ATCGAGGATA TAACGAAGCT CCTTCCGCTAC CAGCTGATTAA TGCCTCAGTC
 74 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAAATC CTTGTGAATT 3900
 75 TAACAGAGGG TATAAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 76 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 77 GAAACGGAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 78 GGAA (end HD-1).

1 28. A recombinant DNA transfer vector comprising
 2 DNA having the following nucleotide sequence or
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 5 sequence:

6 (start HD-73) ATG GATAACAATC 400
 7 CGAACATCAA TGAATGCTATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 8 GAAAGTATTAG GTGGAGAAAG AATAGAAACT GGTACACCC CAATCGATAT 500
 9 TTCCCTTGTG CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGTG
 10 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTGTT TGGTCCCTCT 600
 11 CAATGGGACG CATTCTTG TCAAATTGAA CAGTTAATTAA ACCAAAGAAAT
 12 AGAAGAATTG GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700
 13 ATCTTATCA AATTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT
 14 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 15 CAGTGCCCTT ACAACCGCTA TTCCCTCTTT TGCAGTTCAA AATTATCAAG
 16 TTCCCTCTTT ATCAGTATAT GTTCAAGCTG CAAATTACA TTTATCAGTT 900
 17 TTGAGAGATG TTTCAAGTGTG TGGACAAAGG TGGGGATTG ATGCCGCGAC
 18 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 19 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 20 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAAGAG AATTAACACT 1100
 21 AACTGTATTAA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 22 ATCCAATTG AACAGTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200
 23 GTATTAGAAA ATTTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA
 24 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 25 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAAATA
 26 ATGGCTTCTC CTGTTAGGGTT TTGGGGGCCA GAATTCACTT TTCCGCTATA 1400
 27 TGGAACTATG GGAAATGCGAG CTCCACAAACA ACGTATTGTT GCTCAACTAG
 28 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 29 AATATAGGGAA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAAATT
 30 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 31 GAAACGGTAGA TTGCGTGGAT GAAATACCGC CACAGAAATAA CAACGTGCCA
 32 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTTGTTC 1700
 33 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 34 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900
 35 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTT
 36 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGGACCG 2000
 37 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGBATTCA
 38 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 39 AATTGCGTAC GCTTCTACTA CAAATTACA ATTCCATACA TCAATTGACG

40 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
 41 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTAA
 42 CTTTCAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 43 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 44 ACCTTGAGG CAGAATATGA TTTAGAAAAGA GCACAAAAGG CGGTGAATGA 2400
 45 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 46 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATT 2500
 47 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 48 ACTTAGTGT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
 49 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 50 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 51 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 52 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATASTCAA 2800
 53 GACTTAGAAA TCTATTAAAT TCGCTACAAAT GCAAAACATG AAACAGTAAA
 54 TGTCGCAGGT ACGGGTTCCCT TATGGCCGCT TTCAGCCCCA AGTCCAATCG 2900
 55 GAAAGSTGTGG AGAGCCGAAT CGATGCGCSC CACACCTTGA ATGGAATCCT
 56 GACTTAGATT GTTCGTGTAG GGATGGAGGAA AAGTGTGCC C ATCATTGCA 3000
 57 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 58 TAGGTGTATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 59 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAACGCT
 60 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAT 3200
 61 TGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 62 GCTTTATTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 63 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAACGTT
 64 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGSC TATTTTGAA 3400
 65 GAATTAGAAG GGCCTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 66 TGTCATTAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 67 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTG GGTCTTGT
 68 CTTCCGGAAT GGGAAAGCAGA AGTGTACCAA GAAGTTCGTG TCTGTCCGGG 3600
 69 TCGTGGCTAT ATCCTCGTG TCACAGCGTA CAAGGAGGGG TATGGAGAAG
 70 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700
 71 AGCAACTGCG TAGAAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 72 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 73 ATCGAGGATA TAACGAAAGCT CCTTCCGTAC CAGCTGATT TGCGTCAGTC
 74 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAACG CTTGTGAATT 3900
 75 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 76 AAGAATTAGA ATACTTCCC AAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 77 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA
 78 GGAA (end HD-1).

1 29. The DNA transfer vector of claim 25 trans-
 2 ferred to and replicated in a prokaryotic or lower
 3 eukaryotic microorganism.

1 30. The DNA transfer vector of claim 26 transferred to and replicated in a prokaryotic or lower
2 eukaryotic microorganism.

1 31. The DNA transfer vector of claim 27 transferred to and replicated in a prokaryotic or lower
2 eukaryotic microorganism.

1 32. The DNA transfer vector of claim 28 transferred to and replicated in a prokaryotic or lower
2 eukaryotic microorganism.

1 33. Plasmid pEW1 as shown in FIGURE 1 of the
2 drawings.

1 34. Plasmid pEW2 as shown in FIGURE 2 of the
2 drawings.

1 35. Plasmid pEW3 as shown in FIGURE 3 of the
2 drawings.

1 36. Plasmid pEW4 as shown in FIGURE 4 of the
2 drawings.

1 37. Plasmid PACB-1, having the construction of
2 plasmid pEW3 except that the DNA encoding aspartic
3 acid at position 411 is converted to encode asparagine,
4 and the DNA encoding glycine at position 425 is con-
5 verted to encode glutamic acid.

1 38. Plasmid pSYW1, having the construction of plasmid
2 pEW3 except that the DNA encoding arginine at position
3 289 is converted to encode glycine, the DNA encoding
4 arginine at position 311 is converted to encode lysine,
5 and the DNA encoding tyrosine at position 313 is conver-
6 ted to encode glutamate.

1 39. A microorganism transformed by the transfer
2 vector of claim 25.

1 40. A microorganism transformed by the transfer
2 vector of claim 26.

1 41. A microorganism transformed by the transfer
2 vector of claim 27.

1 42. A microorganism transformed by the transfer
2 vector of claim 28.

1 43. E. coli (pEW3), a microorganism according
2 to claim 39.

1 44. E. coli (pEW4), a microorganism according to
2 claim 40.

1 45. E. coli (pACB-1), a microorganism according
2 to claim 41.

1 46. E. coli (pSYW1), a microorganism according
2 to claim 42.

1 47. A process for preparing pesticidal chimeric
2 toxin EW3 having the following amino acid sequence:

3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I F L F A V
8 Q N Y Q V P F L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y I D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
13 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G

14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
 15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 16 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
 17 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
 18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
 19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
 21 I D G R P I N Q G N F S A T M M S S G S N L Q S G S F R T V G
 22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
 23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
 24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
 25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
 26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
 27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
 28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
 29 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
 30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
 31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
 32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
 33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
 34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
 35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
 36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
 37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
 38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
 39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
 40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
 41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
 42 E L L L M E E

43 which comprises culturing a prokaryotic microbe
 44 hosting a recombinant DNA transfer vector, denoted
 45 pEW3, comprising DNA having the following nucleotide
 46 sequence or equivalent nucleotide sequences containing
 47 bases whose translated region codes for the same
 48 amino acid sequence:

49 (start HD-73) ATG GATAACAATC 400
 50 C G A A C A T C A A T G A A T G C A T T C C T T A T A A T T G T T A A G T A A C C C T G A A G T A 500
 51 G A A G T A T T A G G T G G A G A A A G A A T A G A A A C T G G T T A C A C C C C A A T C G A T A T 600
 52 T T C C T T G T C G C T A A C G C A A T T T C T T T G A G G T G A A T T T G T T C C C G G T G C T G
 53 G A T T T G T G T T A G G A C T A G T T G A T A T A T A T G G G G A A T T T T T G G T C C C T C 700
 54 C A A T G G G A C G C A T T T C T T G T A C A A A T T G A A C A G T T A A T T A A C C C A A A G A A T
 55 A G A A G A A T T C G C T A G G A A C C A A G C C A T T T C T A G A T T A G A A G G A C T A A G C A 800
 56 A T C T T T A T C A A A T T T A C G C A G A A T C T T T A G A G A G T G G G G A A G C A G A T C C T
 57 A C T A A T C C A G C A T T A A G A G A G A G A G A T G C G T A T T C A A T T C A A T G A C A T G A A 900
 58 C A G T G C C C T T A C A A A C C G C T A T T C C T C T T T G G C A G T T C A A A T T T A C A A T T A T C A A G
 59 T T C C T C T T T A T C A G T A T A T G T T C A A G C T G C A A A T T T A C A A T T A T C A G T T 900
 60 T T G A G A G A T G T T C A G T G T T T G G A C A A A G G T G G G G A T T T G A T G C C G C G A C

61 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATAACAG 1000
62 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
63 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
64 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
65 ATCCAATTG AACAGTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200
66 GTATTAGAAA ATTTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA
67 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
68 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA
69 ATGGCTTCTC CTGAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400
70 TGGAACTATG GGAAATGCAG CTCCACAAACA ACGTATTGTT GCTCAACTAG
71 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTT 1500
72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
73 TGCTTATGGG ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
74 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
75 CCTAGGCAAG GATTAGTCA TCGATTAAGC CATGTTCAA TGTTCGTTC 1700
76 AGGCTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
77 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900
78 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
79 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
80 GATTACAGG AGGAGATATT CTTGAAAGAA CTTCACCTGG CCAGATTTC
81 ACCTTAAGAG TAAATATTAC TGACCACTTA TCACAAAGAT ATCGGGTAAG 2100
82 AATTGCTAC GCTTCTACTA CAAATTACA ATTCCATACA TCAATTGACG
83 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
84 AATTTACAGT CCGGAAGCTT TAGGACTGTA GTTTTACTA CTCCGTTAA
85 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
86 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
87 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
88 GCTGTTACT TCTTCAAATC AAATCGGGTT AAAACACAGAT GTGACGGATT
89 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATT 2500
90 TGTCTGGATG AAAAACAAAGA ATTGTCGAG AAAGTCAAAC ATGCGAAGCG
91 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
92 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
93 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
94 TGATGAGTGC TATCCAACGT ATTTATATCA AAAATAGAT GAGTCGAAAT
95 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATASTCAA 2800
96 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
97 TGTGCCAGGT ACGGGTTCCCT TATGGCCGCT TTCAGCCCCA AGTCCAATCG 2900
98 GAAAGTGTGG AGAGCGGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
99 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC CTCATTGCA 3000
100 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
101 TAGGTGATATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
102 CTAGGGAATC TAGAGTTCTC CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
103 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GASAGACAAA CGTGAAGGAA 3200
104 TGGAATGGGA AACAAATATC GTTATATAAG AGGCAAAAGA ATCTGTAGAT
105 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
106 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAACGCTT
107 ATCTGCTGAA GCTGCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400
108 GAATTAGAAG GGCCTATTTC CACTGCATTC TCCCTATATG ATGCGAGAAA
109 TGTCAATTAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
110 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCCCTGTT
111 CTTCCGGAAT GGGAAAGCAGA AGTGTCAACAA GAAGTTCGTG TCTGTCCGGG 3600
112 TCGTGGCTAT ATCCCTCGTG TCACAGCGTA CAAGGAGGGAA TATGGAGAAG
113 GTTGCCTAAC CATTGATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
114 AGCAACTGCG TAGAAGAGGAA AATCTATCCA AATAACACGG TAACGTGTAA

M12C1FDF3D2

115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCCTAC ACTTCTCGTA 3800
116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
117 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAACATC CTTGTGAATT 3900
118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
119 AAGAATTAGA ATACTTCCC AAAACCGATA AGGTATGGAT TGAGATTGGA 4000
120 GAAACCGGAAG GAACATTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA
121 GGAA (end HD-1).

1 48. A process for preparing pesticidal chimeric
2 toxin EW4 having the following amino acid sequence:

3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V
8 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L
13 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G
14 P E F A F F L F G N A G N A A P P V L V S L T G L G I F R T
15 L S S P L Y R R I I L G S G P N N Q E L F V L D G T E F S F
16 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S
17 V P P F R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q
18 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G
19 N F L F N G S V I S G P G F T G G D L V R L N S S G N N I Q
20 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I
21 H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D
22 F G Y F E S A N A F T T S S L G N I V G V R N F S G T A G V I
23 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F
24 T S T N D L G L K T N V T D Y H I D Q V S N L V T Y L S D E
25 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N
26 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N
27 Y V T L S G T F D E C Y P T Y L Y Q K I D E S K L K A F T R
28 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P
29 G T G S L W P L S A Q S P I G K C G E P N R C A P H L E W N
30 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D
31 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E
32 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N
33 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M
34 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F
35 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S
36 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S
37 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H
38 E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y
39 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S
40 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V
41 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D
42 S V E L L L M E E

43 which comprises culturing a prokaryotic microbe
44 hosting a recombinant DNA transfer vector, denoted
45 pEW4, comprising DNA having the following nucleotide
46 sequence or equivalent nucleotide sequences containing
47 bases whose translated region codes for the same amino
48 acid sequence:

49 (start HD-1) ATGG ATAACAATCC GAACATCAAT
 50 GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
 51 TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTGCG
 52 TAACGCAATT TCTTTGAGT GAATTGTTT CCGGTGCTGG ATTGTGTTA 700
 53 GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC
 54 ATTTCCTGTA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTG 800
 55 CTAGGAACCA AGCCATTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
 56 ATTTACGCAG AATCTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
 57 ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCTTA
 58 CAACCGCTAT TCCCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTA 1000
 59 TCAGTATATG TTCAAGCTGC AAATTACAT TTATCAGTT TGAGAGATGT
 60 TTCAGTGTGTT GGACAAASGT GGGGATTGAA TGCCGCGACT ATCAATAGTC 1100
 61 GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTTG
 62 CGCTGGTACA ATACGGGATT AGAGCGTGTAA TGGGGACCAGG ATTCTAGAGA 1200
 63 TTGGGTAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
 64 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTGCA 1300
 65 ACAGTTTCCC AATTAACAAG AGAAATTATG ACGAACCCAG TATTAGAAAA
 66 TTTTGATGGT AGTTTCTGTG GAATGGCTCA GAGAATAAGAA CAGAATATTA 1400
 67 GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCCT TTATACTGAT
 68 GTGCACTAGAG GCTTTAATTAA TTGGTCAGGGG CATCAAATAA CAGCTTCTCC 1500
 69 TGTAGGGTTT TCAGGACCCAG AATTGCGATT CCCTTATTG GGGAAATGCGG
 70 GGAATGCAGC TCCACCCGTA CTTGCTCTCAT TAACTGGTTT GGGGATTGTTT 1600
 71 AGAACATTAT CTTCACCTTT ATATAGAAGA ATTATACTTG GTTCAGGCC
 72 AAATAATCAG GAACTGTTG TCCTTGATGG AACGGAGTTT TCTTTGCGCT 1700
 73 CCCTAACGAC CAACTTGCC TCCACTATAT ATAGACAAAG GGGTACAGTC
 74 GATTCACTAG ATGTAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
 75 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
 76 GAGCAGTTA CACCTTGAGA GCTCAACGT (stop HD-1)
 77 (start HD-73) . CCT ATGTTCTCTT
 78 GGATACATCG TAGTGTGAA TTTAATAATA TAATTCATC GGATAGTATT 1800
 79 ACTCAAATCC CTGCACTGAA GGGAAACTTT CTTTTTAATG GTTCTGTAAT
 80 TTCAGGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
 81 GAAATAACAT TCAGAAATAGA GGGTATAATTG AAGTTCCAAT TCACTTCCCCA
 82 TCGACATCTA CCAGATATCG AGTTCTGTAA CGGTATGCTT CTGTAACCCC 2000
 83 GATTCACTC AACGTTAATT GGGGTAATTG ATCCATTGTT TCCAATACAG
 84 TACCAAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTGGT 2100
 85 TATTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
 86 TGTTAGAAAT TTTAGTGGGA CTGCAAGGAGT GATAATAGAC AGATTTGAAT 2200
 87 TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG

88 CAGAAGGCAGG TGAATGCGCT GTTTACGTCT ACAAAACCAAC TAGGGCTAAA 2300
 89 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
 90 ATTTATCGGA TGAATTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
 91 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTAC TCCAAGATTC
 92 AAATTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCGGAAGTA 2500
 93 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
 94 ACACTATCAG GTACCTTGT TGAGTGTCTAT CCAACATATT TGTATCAAAA 2600
 95 AATCGATGAA TCAAAAATTAA AAGCCTTAC CCGTTATCAA TTAAGAGGGT
 96 ATATCGAAGA TAGTCAAGAC TTAGAAAATCT ATTTAATTGCA CTACAATGCA 2700
 97 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTTAT GGCGCGCTTC
 98 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCGCGCCAC 2800
 99 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGAA TGGAGAAAAG
 100 TGTGCCCATC ATTTCGATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900
 101 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 102 AAGATGGGCA CGCAAGACTA GGGAAATCTAG AGTTTCTCGA AGAGAAAACCA 3000
 103 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 104 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAAGAGG 3100
 105 CAAAAGAACATC TGAGATGCT TTATTGTAAG ACTCTCAATA TGATCAATT
 106 CAAGCGGATA CGAATATTGCA CATGATTATC GCGGCAGATA AACGTGTTCA 3200
 107 TAGCATTCGA GAAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA
 108 ATGCGGCTAT TTTTGAAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300
 109 CTATATGATG CGAGAAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT
 110 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTTAGAAGAA CAAAACAACC 3400
 111 AACGTTCGGT CCTTGTGTT CCGGAATGGG AAGCAGAAAGT GTCACAAGAA
 112 GTTCGTGTCT GTCCGGGTCTG TGGCTATATC CTTCGTGTCA CAGCGTACAA 3500
 113 GGAGGGATAT GGAGAAGGTG GCGTAACCAT TCATGAGATC GAGAACAAATA
 114 CABACGAACT GAAAGTTTAGC AACTCGTAG AAGAGGAAAT CTATCCAAT 3600
 115 AACACGGTAA CGTGTAAATGA TTATACTGTA AATCAAGAAG AATACGGAGG
 116 TGCCTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAAG 3700
 117 CTGATTATGC GTCACTGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAAGA
 118 GAGAATCCTT GTGAATTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 119 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCCAGAA ACCGATAAGG
 120 TATGGATTGA GATTGGAGAA ACGGAAAGGAA CATTATCGT GGACAGCGTG 3900
 121 GAATTACTCC TTATGGAGGA A (end HD-73).

1 49. A process for preparing pesticidal chimeric
 2 toxin ACB-1 having the following amino acid sequence:

3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
 4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 5 V D I I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
 6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
 8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
 9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
 12 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
 13 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
 14 P E F T F F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R

15 TLSSTLYRPFNIGINNQQLSVLDGTEFA
16 GTSSNLPSAVYRKSGTVDSLNEIPPQNNNV
17 PPRQEFSHRLSHVSMFRSGFSNSSVSIIRA
18 PTFSWQHRSAEFNNIIPSSQITQIPLTKST
19 NLGSGTSVVKGPFGTGGDILRRTSPGQIST
20 LRVNITAPLSQRYRVRIRYASTTNLQFHTS
21 IDGRPINQGNFSATMSSGSNLQSGSFRTVG
22 FTTPFNFNSNGSSVFTLSAHVFNSGN
23 RIEFVPAEVTFEAEYDLEERAQKAVNELFTS
24 SNQIGLKTDVTDYHIDQVSNLVECLSDEF
25 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
26 GINRQLDRGWRGSTDITIQQGDDVFKENYV
27 TLLGTFDECYPTLYQKIDESKLKAYTRYQ
28 LRGYIEDSQDLEIYLI
29 GSLWPLSAQSP
30 LDCSCRDG
31 EDLGVWVI
32 LVGEALARVKRAEKKWRDKREKLE
33 YKEAKESVD
34 AADKRVHS
35 LEGRI
36 NVKG
37 VRVC
38 ENNT
39 NQE
40 EEKSY
41 VTKELEY
42 ELLLMEE

43 which comprises culturing a prokaryotic microbe
44 hosting a recombinant DNA transfer vector, denoted
45 PACB-1, comprising DNA having the following nucleotide
46 sequence or equivalent nucleotide sequences containing
47 bases whose translated region codes for the same
48 amino acid sequence:

49 (start HD-73) ATG GATAACAATC 400
50 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
51 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500
52 TTCCCTGTG CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGCTG
53 GATTGTTAGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
54 CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAATTA ACCAAAGAAT
55 AGAAGAATTC GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700
56 ATCTTTATCA AATTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT
57 ACTAATCCAG CATTAAAGAGA AGAGATGCCT ATTCAATTCA ATGACATGAA 800
58 CAGTGCCCTT ACAACCGCTA TTCCCTTTT TGCAGTTCAA AATTATCAAG
59 TTCCCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
60 TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTTG ATGCCGCGAC

61 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
62 ATTATGCTGT ACGCTGGTAC AATAACGGGAT TAGAACGTGT ATGGGGACCG
63 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
64 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
65 ATCCAATTG AACAGTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200
66 GTATTAGAAA ATTTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA
67 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
68 TCTATACGGG TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAAATA
69 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400
70 TGGAACATAG GGAAATGCAG CTCCACAAACA ACGTATTGTT GCTCAACTAG
71 GTCAGGGCGT GTATAGAAC TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
73 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
74 GAACGGTAGA TTCGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA
75 CCTAGGCAAG AATTAGTCA TCGATTAAGC CATGTTCAA TGTTTCGTT 1700
76 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
77 (start HD-1) CCAADGT TTTCTTGGCA GCATCGCACT 1900
78 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
79 AACAAAATCT ACTAATCTTG GCTCTGAAAC TTCTGTCGTT AAAGGACCG 2000
80 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTCA
81 ACCTTAAGAG TAAATATTAC TGCAACATTAA TCACAAAGAT ATCGGGTAAG 2100
82 AATTCGCTAC GCTTCTACTA CAAATTACA ATTCACATACA TCAATTGACG
83 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
84 AATTTACAGT CCGGAAGCTT TAGGACTGTA GTTTTACTA CTCCGTTAA
85 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCCTAT GTCTTCATT 2300
86 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAAGAGTA
87 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
88 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
89 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATT 2500
90 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
91 ACTTAGTGTG GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
92 ATAGACAACT AGACCGTGGC TGGAGAGGAA STACGGATAT TACCATCCAA
93 GGAGGCAGTG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
94 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
95 TAAAAGCCTA TACCCGTTAT CAATTAAAGAG GGTATATCGA AGATAGTCAA 2800
96 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACASTAAA
97 TGTGCCAGGT ACGGGTTCT TATGGCCGCT TTCAAGCCCAA AGTCCAATCG 2900
98 GAAAGTGTGG AGAGCGGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
99 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC CTCATTGCA 3000
100 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
101 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
102 CTAGGGAAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
103 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTGAAGAAAT 3200
104 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
105 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
106 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAAGCTT
107 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400
108 GAATTAGAAG GGCGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAAA
109 TGTCAATTAAA AATGGGTGATT TTAATAATGG CTTATCCTGCG TGGAACGTGA 3500
110 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCTTGTT
111 CTTCCGGAAT GGGAAAGCGAGA AGTGTACCAA GAAGTTCGTG TCTGTCCGGG 3600
112 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG

113 GTTGCCTAAC CATTGAGATCGAGAACATACAGACGA ACTGAAGTTT 3700
114 AGCAACTGCG TAGAAGAGGAA AATCTATCCA AATAACACGG TAACGCTGTA
115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATT TGCGTCAGTC
117 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
118 TAACAGAGGG TATAAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
120 GAAACGGAAG GAAACATTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA
121 GGAA (end HD-1).

1 50. A process for preparing pesticidal chimeric
2 toxin SYW1 having the following amino acid sequence:

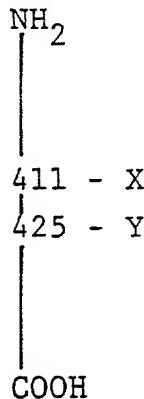
3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L
13 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G
14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
16 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
17 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
18 P T F S W Q H R S A E F N N I I F S S Q I T Q I P L T K S T
19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
21 I D G R P I N Q G N F S A T M M S S G S N L Q S G S F R T V G
22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
26 S I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V F G T
29 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
31 E D L G V W V I F K I K T Q D G H A R L G N L E F F L E E K P
32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
42 E L L L M E E

43 which comprises culturing a prokaryotic microbe
44 hosting a recombinant DNA transfer vector, denoted
45 pSYW1, comprising DNA having the following nucleotide
46 sequence or equivalent nucleotide sequences containing
47 bases whose translated region codes for the same
48 amino acid sequence:

49 (start HD-73) ATG GATAACAATC 400
50 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
51 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTACACCCC CAATCGATAT 500
52 TTCCCTGTCG CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGCTG
53 GATTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTC TGGTCCCTCT 600
54 CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAATTAA ACCAAAGAAT
55 AGAAGAATTG GCTAGGAACC AABCCATTC TAGATTAGAA GGACTAAGCA 700
56 ATCTTATCA AATTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT
57 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
58 CAGTGCCCTT ACAACCGCTA TTCCCTTTT TGCAGTTCAA AATTATCAAG
59 TTCCCTCTTT ATCAGTATAT GTTCAAGCTG CAAATTACA TTTATCAGTT 900
60 TTGAGAGATG TTTCACTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
61 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
62 ATTATGCTGT ACGCTGGTAC AATAACGGGAT TAGAACGTGT ATGGGGACCG
63 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTAGAAAGAG AATTAACACT 1100
64 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAAGAT
65 ATCCAATTGCG AACAGTTTCC CAATTAACAA GAGAAATTAA TACAAAACCCA 1200
66 GTATTAGAAA ATTTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA
67 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
68 TCTATACGGA TGCTCATAAA GGGGAATATT ATGGGTCAAGG SCATCAAATA
69 ATGGCTTCTC CTGTAAGGGTT TTCCGGGCCA GAATTCACTT TTCCGCTATA 1400
70 TGGAACTATG GGAATGCAAG CTCCACAAACA ACGTATTGTT GCTCAACTAG
71 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
73 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
74 GAAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
75 CCTAGGCAAG GATTAGTCA TCGATTAAAGC CATGTTCAA TGTTCGTT 1700
76 AGGCTTTAGT AATAGTGTG TAAGTATAAT AAGAGCT (end hd-73)
77 (start HD-1) CCAACGT TTTCTGGCA SCATCGCACT 1900
78 GCTGAATTAA ATAATATAAT TCCCTTCATCA CAAATTACAC AAATACCTTT
79 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
80 GATTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTCA
81 ACCTTAAGAG TAAATATTAC TGCAACATTA TCACAAAGAT ATCGGGTAAG 2100
82 AATTGCTAC GCTTCTACTA CAAATTACA ATTCCATACCA TCAATTGACG
83 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
84 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTACTA CTCCGTTAA
85 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
86 CAGGCAATGA AGTTTATATA GATCGAATTG AATTGTTCC GGCAGAAAGTA
87 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
88 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
89 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTGTTATC AGATGAATT 2500
90 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
91 ACTTAGTGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
92 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA

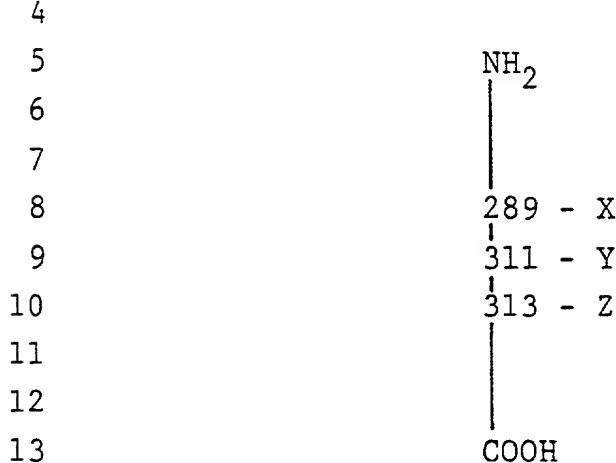
93	GGAGGCGATG	ACGTATTCAA	AGAGAATTAC	GTTACGCTAT	TGGGTACCTT	2700
94	TGATGAGTGC	TATCCAACGT	ATTATATATCA	AAAAATAGAT	GAGTCGAAAT	
95	TAAAAGCCTA	TACCCGTTAT	CAATTAAGAG	GGTATATCGA	AGATAGTCAA	2800
96	GACTTAGAAA	TCTATTAAAT	TCGCTACAAT	GCAAAACATG	AAACAGTAAA	
97	TGTGCCAGGT	ACGGGTTCCCT	TATGGCCGCT	TTCAAGCCAA	AGTCCAATCG	2900
98	GAAAGTGTGG	AGAGCCGAAT	CGATGCGCGC	CACACCTTGA	ATGGAATCCT	
99	GACTTAGATT	GTTCGTGTAG	GGATGGAGAA	AAGTGTGCC	ATCATTCGCA	3000
100	TCATTTCTCC	TTAGACATTG	ATGTAGGATG	TACAGACTTA	AATGAGGACC	
101	TAGGTGTATG	GGTGTCTTT	AAGATTAAGA	CGCAAGATGG	GCACGCAAGA	3100
102	CTAGGGAATC	TAGAGTTTCT	CGAAGAGAAA	CCATTAGTAG	GAGAAGCGCT	
103	AGCTCGTGTG	AAAAGAGCGG	AGAAAAAAATG	GAGAGACAAA	CGTAAAAAAAT	3200
104	TGGAATGGGA	AACAAATATC	GTTTATAAAG	AGGCAAAAGA	ATCTGTAGAT	
105	GCTTTATTG	TAACACTCTCA	ATATGATCAA	TTACAAGCGG	ATACGAATAT	3300
105	TGCCATGATT	CATGCGGCCAG	ATAAACGTGT	TCATAGCATT	CGAGAAGCTT	
107	ATCTGCCTGA	GCTGTCTGTG	ATTCGGGTG	TCAATGCGGC	TATTTTTGAA	3400
108	GAATTAGAAG	GGCGTATTTT	CACTGCAATTC	TCCCTATATG	ATGCGAGAAA	
109	TGTCATTAAA	AATGGTGATT	TTAATAATGG	CTTATCCTGC	TGGAACGTGA	3500
110	AAGGGCATGT	AGATGTAGAA	GAACAAAAAC	ACCAACGTTT	GGTCCTTGT	
111	CTTCGGAAAT	GGGAAGCAGA	AGTGTACCAA	GAAGTTCGTG	TCTGTCCGGG	3600
112	TCGTGGCTAT	ATCCTTCGTG	TCACAGCGTA	CAAGGAGGGG	TATGGAGAAG	
113	GTTGCGTAAC	CATTGATGAG	ATCGAGAAC	ATACAGACGA	ACTGAAGTT	3700
114	AGCAACTGCG	TAGAAGAGGA	AATCTATCCA	AATAACACGG	TAACGTGTAA	
115	TGATTATACT	GTAAATCAAG	AAGAATACGG	AGGTGCGTAC	ACTTCTCGTA	3800
116	ATCGAGGATA	TAACGAAGCT	CCTTCCGTAC	CAGCTGATT	TGCGTCAGTC	
117	TATGAAGAAA	AATCGTATAC	AGATGGACGA	AGAGAGAAC	CTTGTGAATT	3900
118	TAACAGAGGG	TATAGGGATT	ACACGCCACT	ACCAAGTTGGT	TATGTGACAA	
119	AAGAATTAGA	ATACTTCCCA	GAAACCGATA	AGGTATGGAT	TGAGATTGGA	4000
120	GAAACGGAAG	GAACATTAT	CGTGGACAGC	GTGGAAATTAC	TCCTTATGGA	
121	GGAA	(end HD-1).				

1 51. A chimeric toxin, having the amino acid
2 sequence of toxin EW3, with changes which can be shown
3 schematically as follows:



13 wherein X is one of the 20 common amino acids
14 except Asp when the amino acid at position 425 is
15 Gly; Y is one of the 20 common amino acids except
16 Gly when the amino acid at position 411 is Asp.

1 52. A chimeric toxin, having the amino acid
2 sequence of toxin EW3, with changes which can be shown
3 schematically as follows:



15 wherein X is one of the 20 common amino acids except
16 Arg when the amino acid at position 311 is Arg and the
17 amino acid at position 313 is Tyr; Y is one of the 20
18 common amino acids except Arg when the amino acid at
19 position 289 is Arg and the amino acid at position 313
20 is Tyr; and Z is one of the 20 common amino acids
21 except Tyr when the amino acid at position 289 is
22 Arg and the amino acid at position 311 is Arg.

1 53. DNA encoding a chimeric toxin as shown in
2 claim 51.

1 54. DNA encoding a chimeric toxin as shown in
2 claim 52.

1 55. A recombinant DNA transfer vector comprising
2 DNA encoding a chimeric toxin as shown in claim 51.

1 56. A recombinant DNA transfer vector comprising
2 DNA encoding a chimeric toxin as shown in claim 52.

1 57. A chimeric toxin comprising the variable
2 region or regions of two or more Bacillus toxins.

1 58. A toxin, according to claim 57, wherein the
2 Bacillus toxins are B. thuringiensis toxins.

1 59. A toxin, according to claim 58, wherein the
2 B. thuringiensis toxins are B. thuringiensis var.
3 kurstaki HD-1 toxin and B. thuringiensis var. kurstaki
4 HD-73 toxin.

1 60. A toxin, according to claim 58, wherein
2 the B. thuringiensis toxins are encoded by a pesticide-
3 producing strain of Bacillus thuringiensis, consisting
4 of B. thuringiensis M-7, B. thuringiensis var. kurstaki,
5 B. thuringiensis var. finitimus, B. thuringiensis var.
6 alesti, B. thuringiensis var. sotto, B. thuringiensis
7 var. dendrolimus, B. thuringiensis var. kenyae, B.
8 thuringiensis var. galleriae, B. thuringiensis var.
9 canadensis, B. thuringiensis var. entomocidus, B.
10 thuringiensis var. subtoxicus, B. thuringiensis var.
11 aizawai, B. thuringiensis var. morrisoni, B. thuringiensis
12 var. ostriniae, B. thuringiensis var. tolworthi, B.
13 thuringiensis var. darmstadiensis, B. thuringiensis
14 var. toumanoffi, B. thuringiensis var. kyushuensis, B.
15 thuringiensis var. thompsoni, B. thuringiensis var.
16 pakistani, B. thuringiensis var. israelensis, B. thurin-
17 giensis var. indiana, B. thuringiensis var. dakota,

18 B. thuringiensis var. tohokuensis, B. thuringiensis
19 var. kumanotoensis, B. thuringiensis var. tochigiensis,
20 B. thuringiensis var. colmeri, B. thuringiensis var.
21 wuhanensis, B. thuringiensis var. tenebrionis, B.
22 thuringiensis var. thuringiensis, and other Bacillus
23 species selected from B. cereus, B. moritai, B.
24 popilliae, B. lentimorbus, and B. sphaericus.